52

Raw Sequence Listing

Au 1806

Patent Application US/07/952,640

1 2		SEQUENCE LISTING
3		8 00
4	(1) GENE	ral information:
5 6 7 8	(i)	APPLICANT: CROWE, JAMES SCOTT LEWIS, ALAN PETER
9 10	(ii)	TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
11 12	(iii)	NUMBER OF SEQUENCES: 46
13 14 15 16 17 18 19 20		CORRESPONDENCE ADDRESS: (A) ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ (B) STREET: 555 THIRTEENTH ST. N.W. (C) CITY: WASHINGTON (D) STATE: D. C. (E) COUNTRY: U.S. (F) ZIP: 20004
21 22 23 24 25 26	, , ,	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27 28 29 30 31	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: US 07/952640 (B) FILING DATE: 01-DEC-1992 (C) CLASSIFICATION:
32 33 34 35 36	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: ERNST, BARBARA G (B) REGISTRATION NUMBER: 30,377 (C) REFERENCE/DOCKET NUMBER: 1808-118
37 38 39 40 41	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (202) 783-6040 (B) TELEFAX: (202) 783-6031
42	(2) INF	ORMATION FOR SEQ ID NO:1:
44 45 46 47 48 49		SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
50 51	(ii)	MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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53 54	GACATTCAGC TGACCCAGTC TCCA	24
55		
56 57	(2) INFORMATION FOR SEQ ID NO:2:	
58	(i) SEQUENCE CHARACTERISTICS:	
59	(A) LENGTH: 24 base pairs	
60	(B) TYPE: nucleic acid	
61	(C) STRANDEDNESS: single	
62	(D) TOPOLOGY: linear	
63		
64	(ii) MOLECULE TYPE: DNA (genomic)	
65		
66	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
67		
68	GATCAAGCTT CTAACACTCT CCCC	24
69 70	(2) THEODYSMION BOD GEO ID NO.2.	
71	(2) INFORMATION FOR SEQ ID NO:3:	
72	(i) SEQUENCE CHARACTERISTICS:	
73	(A) LENGTH: 34 base pairs	
74	(B) TYPE: nucleic acid	
75	(C) STRANDEDNESS: single	
76	(D) TOPOLOGY: linear	
77		
78	(ii) MOLECULE TYPE: DNA (genomic)	
79		
80	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
81		
82	GATCAAGCTT GACATTCAGC TGACCCAGTC TCCA	34
83	/0\	
84	(2) INFORMATION FOR SEQ ID NO:4:	
85 86	(i) SEQUENCE CHARACTERISTICS:	
87	(A) LENGTH: 16 base pairs	
88	(B) TYPE: nucleic acid	
89	(C) STRANDEDNESS: single	
90	(D) TOPOLOGY: linear	
91		
92	(ii) MOLECULE TYPE: DNA (genomic)	
93		
94	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
95	\cdot	
96	AACAGCTATG ACCATG	16
97	(A) TYPODYARTON FOR STO TR NO F	
98 99	(2) INFORMATION FOR SEQ ID NO:5:	
99 100	(i) SEQUENCE CHARACTERISTICS:	
101	(A) LENGTH: 17 base pairs	
102	(B) TYPE: nucleic acid	
103	(C) STRANDEDNESS: single	
104	(D) TOPOLOGY: linear	
- -		

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105		
105	(ii) MOLECULE TYPE: DNA (genomic)	
107	(II) MODECODE IIPE: DNA (Genomic)	
108	(wi) CENTENCE DECERTATION, CENT TO NO.E.	
103	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
110		17
111	GTTTTCCCAG TCACGAC	1/
	(0) TYPODY MICH DOD GOO TO NO.C.	
112 113	(2) INFORMATION FOR SEQ ID NO:6:	
113	(4) GEOVERIGE GUADAGMEDTGMEGG.	
114	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs	
116	•	
117	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
118 119	(D) TOPOLOGI: linear	
	(ii) NOI EGUI E MUDE. DVA (comomic)	
120	(ii) MOLECULE TYPE: DNA (genomic)	
121	(
122 123	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
123	GCGTCAGGGT GCTGCTGAGG	20
125	GCGTCAGGGT GCTGCTGAGG	20
125	(2) INFORMATION FOR SEQ ID NO:7:	
127	(2) INFORMATION FOR SEQ ID NO:/:	
128	(i) SEQUENCE CHARACTERISTICS:	
129	(A) LENGTH: 20 base pairs	
130	(B) TYPE: nucleic acid	
131	(C) STRANDEDNESS: single	
132	(D) TOPOLOGY: linear	
133	(D) TOPOLOGI: IINBAI	
134	(ii) MOLEGULE MUDE. DNA (conomic)	
135	(ii) MOLECULE TYPE: DNA (genomic)	
136	() CENTENCE DESCRIPTION, SEC ID NO.7.	
137	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
138	GGCGGGAAGA TGAAGACAGA	20
139	GGCGGAAGA IGAAGACAGA	20
140	(2) INFORMATION FOR SEQ ID NO:8:	
141	(2) INFORMATION FOR BEQ ID NO:0:	
142	(i) SEQUENCE CHARACTERISTICS:	
143	(A) LENGTH: 20 base pairs	
144	(B) TYPE: nucleic acid	
145	(C) STRANDEDNESS: single	
146	(D) TOPOLOGY: linear	
147	(b) loronogi. linear	
148	(ii) MOLECULE TYPE: DNA (genomic)	
149	(II) MODECODE IIFE. DAN (Genomic)	
150		
151		
151	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
153	/YI) DEGOSMOS DESCRIFITON, DEG ID NO.0:	
154	TTCAGCAGGC ACACAACAGA	20
155	11CHOCHOC ACACAMANA	20
156	(2) INFORMATION FOR SEQ ID NO:9:	
730	(2) INFORMATION FOR SEQ 10 NO.5.	

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158		(i)) SE	QUEN	CE C	HARA	CTER	ISTI	CS:								
159			(2	A) L	ENGT	H: 1	517]	base	pai:	rs							
160			(1	B) T	YPE:	nuc.	leic	aci	ď								
161			((C) S:	TRAN	DEDN	ESS:	bot	h								
162			(1) T	OPOL	OGY:	lin	ear									
163																	
164		(ii)	MO:	LECU	LE T	YPE:	cDN	A									
165														r			
166		(iii)	HY	POTH	ETIC	AL: 1	O 7										
167																	
168		(iv	AN'	ri-si	ense	: NO											
169																	
170																	
171		(ix)	FE														
172					AME/I				tide								
173			(1	3) L(OCAT:	CON:	35.	.92									
174																	
175		(ix	FE														
176					AME/I		-										
177			(1	3) L(OCAT:	CON:	93.	.146	5								
178																	
179		(ix)) FE														
180					AME/I												
181			(1	3) L(CAT:	CON:	35.	. 146	5								
182																	
183																	
184			077		an -	300n		N	750		^ - ^ -						
105		(xi	SE	QUEN	CE DI	ESCR:	[PTI	ON:	SEQ :	ID N	0:9:						
185	ጥርሞን			•					_			N C' 117/	7C N	70 m	CC 3/	70	52
186	TCT	(xi) AAAG		•					_	CC A	rg g						52
186 187	TCT			•					_	CC A'	TG G			hr T	rp A		52
186 187 188	TCT			•					_	CC A'	rg g			hr T			52
186 187 188 189		AAAG	AAG (ccc:	rggg	AG CI	ACAG	CTCA:	r CA	CC AS	TG G et A 19	sp T	rp Tl	nr T: -:	rp A: 15	rg	
186 187 188 189 190	TTC	AAAG CTC	AAG (CCCC GTG	rggg; Gtg	AG CZ GCA	ACAG(GCA	CTCA:	r ca	CC A' Me -: GGT	TG G et A 19 GTC	SP T	rp Tl TCC	nr T: -: CAG	rp A: 15 ATG	rg CAG	52 100
186 187 188 189 190	TTC	AAAG	AAG (GTG Val	rggg; Gtg	AG CZ GCA	ACAG(GCA	CTCA:	CACA Thr	CC A' Me -: GGT	TG G et A 19 GTC	SP T	rp Tl TCC	CAG	rp A: 15 ATG	rg CAG	
186 187 188 189 190 191	TTC	AAAG CTC	AAG (CCCC GTG	rggg; Gtg	AG CZ GCA	ACAG(GCA	CTCA:	r ca	CC A' Me -: GGT	TG G et A 19 GTC	SP T	rp Tl TCC	nr T: -: CAG	rp A: 15 ATG	rg CAG	
186 187 188 189 190	TTC Phe	AAAG CTC	AAG (TTT Phe	GTG Val	rggg grg Val	AG CA GCA Ala	ACAGO GCA Ala	GCT Ala	ACA Thr	MG -: GGT Gly	rg ga et Aa 19 GTC Val	CAG Gln	TCC Ser	CAG Gln 1	rp A 15 ATG Met	cag Gln	
186 187 188 189 190 191 192 193	TTC Phe GTG	CTC Leu GTG	TTT Phe	GTG Val -10	GTG Val	GCA Ala GCT	GCA Ala GAA	GCT Ala GTA	ACA Thr -5	GGT GGT GAG	rg great Ar 19 GTC Val	CAG Gln GGG	TCC Ser	CAG Gln 1	rp A: 15 ATG Met GTG	CAG Gln ACG	100
186 187 188 189 190 191 192 193 194	TTC Phe GTG	AAAGA CTC Leu	TTT Phe	GTG Val -10	GTG Val	GCA Ala GCT	GCA Ala GAA	GCT Ala GTA	ACA Thr -5	GGT GGT GAG	rg great Ar 19 GTC Val	CAG Gln GGG	TCC Ser	CAG Gln 1	rp A: 15 ATG Met GTG	CAG Gln ACG	100
186 187 188 189 190 191 192 193 194 195	TTC Phe GTG	CTC Leu GTG Val	TTT Phe	GTG Val -10	GTG Val	GCA Ala GCT	GCA Ala GAA Glu	GCT Ala GTA	ACA Thr -5	GGT GGT GAG	rg great Ar 19 GTC Val	CAG Gln GGG Gly	TCC Ser	CAG Gln 1	rp A: 15 ATG Met GTG	CAG Gln ACG	100
186 187 188 189 190 191 192 193 194 195	TTC Phe GTG Val	CTC Leu GTG Val	TTT Phe CAG	GTG Val -10 TCT Ser	GTG Val GGG Gly	GCA Ala GCT Ala	GCA Ala GAA Glu 10	GCT Ala GTA Val	ACA Thr -5 AAG	GGT GGT GLY AAG	rg Gi et Ai 19 GTC Val CCT Pro	CAG Gln GGG Gly 15	TCC Ser TCC Ser	CAG Gln 1 TCG Ser	TP ATG Met GTG Val	CAG Gln ACG Thr	100
186 187 188 189 190 191 192 193 194 195 196	TTC Phe GTG Val	CTC Leu GTG Val	TTT Phe CAG Gln	GTG Val -10 TCT Ser	GTG Val GGG Gly GCA	GCA Ala GCT Ala	GCA Ala GAA Glu 10	GCT Ala GTA Val	ACA Thr -5 AAG Lys	GGT GGT Gly AAG Lys	rg Gi et Ai 19 GTC Val CCT Pro	CAG Gln GGG Gly 15	TCC Ser TCC Ser	CAG Gln 1 TCG Ser	ATG Met GTG Val	CAG Gln ACG Thr	100 148
186 187 188 189 190 191 192 193 194 195 196 197	TTC Phe GTG Val	CTC Leu GTG Val 5	TTT Phe CAG Gln	GTG Val -10 TCT Ser	GTG Val GGG Gly GCA	GCA Ala GCT Ala	GCA Ala GAA Glu 10	GCT Ala GTA Val	ACA Thr -5 AAG Lys	GGT GGT Gly AAG Lys	rg Gi et Ai 19 GTC Val CCT Pro	CAG Gln GGG Gly 15	TCC Ser TCC Ser	CAG Gln 1 TCG Ser	ATG Met GTG Val	CAG Gln ACG Thr	100 148
186 187 188 189 190 191 192 193 194 195 196 197 198	TTC Phe GTG Val GTC Val	CTC Leu GTG Val 5	TTT Phe CAG Gln	GTG Val -10 TCT Ser	GTG Val GGG Gly GCA	GCA Ala GCT Ala TCT Ser	GCA Ala GAA Glu 10	GCT Ala GTA Val	ACA Thr -5 AAG Lys	GGT GGT Gly AAG Lys	GTC Val	CAG Gln GGG Gly 15	TCC Ser TCC Ser	CAG Gln 1 TCG Ser	ATG Met GTG Val	CAG Gln ACG Thr	100 148
186 187 188 189 190 191 192 193 194 195 196 197 198 199 200	TTC Phe GTG Val GTC Val 20	CTC Leu GTG Val 5	TTT Phe CAG Gln TGC Cys	GTG Val -10 TCT Ser	GTG Val GGG Gly GCA Ala	GCA Ala GCT Ala TCT Ser 25	GCA Ala GAA Glu 10 GGA Gly	GCT Ala GTA Val GGC Gly	ACA Thr -5 AAG Lys ACC Thr	GGT GGT Gly AAG Lys TTC	GTC Val CCT Pro AGC Ser	CAG Gln GGG Gly 15 AAC Asn	TCC Ser TCC Ser TAT Tyr	CAG Gln 1 TCG Ser GCT Ala	TP ATG Met GTG Val	CAG Gln ACG Thr AGC Ser 35	100 148
186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201	TTC Phe GTG Val GTC Val 20	CTC Leu GTG Val 5	TTT Phe CAG Gln TGC Cys	GTG Val -10 TCT Ser AAG Lys	GTG Val GGG Gly GCA Ala	GCA Ala GCT Ala TCT Ser 25	GCA Ala GAA Glu 10 GGA Gly	GCT Ala GTA Val GGC Gly	ACA Thr -5 AAG Lys ACC Thr	GGT GGT Gly AAG Lys TTC Phe	GTC Val CCT Pro AGC Ser 30 GAG	CAG Gln GGG Gly 15 AAC ABN	TCC Ser TCC Ser TAT Tyr	CAG Gln 1 TCG Ser GCT Ala	ATG Met GTG Val	CAG Gln ACG Thr AGC Ser 35	100 148 196
186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202	TTC Phe GTG Val GTC Val 20	CTC Leu GTG Val 5 TCC Ser	TTT Phe CAG Gln TGC Cys	GTG Val -10 TCT Ser AAG Lys	GTG Val GGG Gly GCA Ala	GCA Ala GCT Ala TCT Ser 25	GCA Ala GAA Glu 10 GGA Gly	GCT Ala GTA Val GGC Gly	ACA Thr -5 AAG Lys ACC Thr	GGT GGT Gly AAG Lys TTC Phe	GTC Val CCT Pro AGC Ser 30 GAG	CAG Gln GGG Gly 15 AAC ABN	TCC Ser TCC Ser TAT Tyr	CAG Gln 1 TCG Ser GCT Ala	ATG Met GTG Val	CAG Gln ACG Thr AGC Ser 35	100 148 196
186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203	TTC Phe GTG Val GTC Val 20 TGG Trp	CTC Leu GTG Val 5 TCC Ser GTG Val	TTT Phe CAG Gln TGC Cys	GTG Val -10 TCT Ser AAG Lys	GTG Val GGG Gly GCA Ala GCC Ala 40	GCA Ala GCT Ala TCT Ser 25 CCT	GCA Ala GAA Glu 10 GGA Gly GGA	GCT Ala GTA Val GGC Gly CAA Gln	ACA Thr -5 AAG Lys ACC Thr	GGT Gly AAG Lys TTC Phe CTT Leu 45	GTC Val CCT Pro AGC Ser 30 GAG Glu	CAG Gln GGG Gly 15 AAC ABN	TCC Ser TCC Ser TAT Tyr	CAG Gln 1 TCG Ser GCT Ala	ATG Met GTG Val ATC Ile GGG Gly 50	CAG Gln ACG Thr AGC Ser 35 ATC	100 148 196
186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206	TTC Phe GTG Val GTC Val 20 TGG Trp	CTC Leu GTG Val TCC Ser GTG Val	TTT Phe CAG Gln CCys CGA Arg	GTG Val -10 TCT Ser AAG Lys	GTG Val GGG Gly GCA Ala GCC Ala 40	GCA Ala GCT Ala TCT Ser 25 CCT Pro	GCA Ala GAA Glu 10 GGA Gly GGA Gly	GCT Ala GTA Val GGC Gly CAA Gln	ACA Thr -5 AAG Lys ACC Thr GGG Gly	GGT Gly AAG Lys TTC Phe CTT Leu 45	GTC Val CCT Pro AGC Ser 30 GAG GLU CAG	CAG Gln GGG Gly 15 AAC Asn TGG Trp	TCC Ser TCC Ser TAT Tyr ATG Met	CAG Gln 1 TCG Ser GCT Ala GGA Gly	ATG Met GTG Val ATC Ile GGG Gly 50 GGC	CAG Gln ACG Thr AGC Ser 35 ATC Ile	100 148 196
186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207	TTC Phe GTG Val GTC Val 20 TGG Trp	CTC Leu GTG Val 5 TCC Ser GTG Val	TTT Phe CAG Gln TGC Cys CGA Arg	GTG Val -10 TCT Ser AAG Lys	GTG Val GGG Gly GCA Ala GCC Ala 40	GCA Ala GCT Ala TCT Ser 25 CCT Pro	GCA Ala GAA Glu 10 GGA Gly GGA Gly	GCT Ala GTA Val GGC Gly CAA Gln	ACA Thr -5 AAG Lys ACC Thr GGG Gly	GGT Gly AAG Lys TTC Phe CTT Leu 45	GTC Val CCT Pro AGC Ser 30 GAG GLU CAG	CAG Gln GGG Gly 15 AAC Asn TGG Trp	TCC Ser TCC Ser TAT Tyr ATG Met	CAG Gln 1 TCG Ser GCT Ala GGA Gly	ATG Met GTG Val ATC Ile GGG Gly 50 GGC	CAG Gln ACG Thr AGC Ser 35 ATC Ile	100 148 196 244
186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206	TTC Phe GTG Val GTC Val 20 TGG Trp	CTC Leu GTG Val TCC Ser GTG Val	TTT Phe CAG Gln TGC Cys CGA Arg	GTG Val -10 TCT Ser AAG Lys	GTG Val GGG Gly GCA Ala GCC Ala 40	GCA Ala GCT Ala TCT Ser 25 CCT Pro	GCA Ala GAA Glu 10 GGA Gly GGA Gly	GCT Ala GTA Val GGC Gly CAA Gln	ACA Thr -5 AAG Lys ACC Thr GGG Gly	GGT Gly AAG Lys TTC Phe CTT Leu 45	GTC Val CCT Pro AGC Ser 30 GAG GLU CAG	CAG Gln GGG Gly 15 AAC Asn TGG Trp	TCC Ser TCC Ser TAT Tyr ATG Met	CAG Gln 1 TCG Ser GCT Ala GGA Gly	ATG Met GTG Val ATC Ile GGG Gly 50 GGC	CAG Gln ACG Thr AGC Ser 35 ATC Ile	100 148 196 244

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209																	
210		ACG															340
211	Val	Thr		Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	His	Met	Glu	Leu	
212			70					75					80				
213																	
214		AGC															388
215	Thr	Ser	Leu	Arg	Ser	Glu		Thr	Ala	Val	Tyr		Сув	Ala	Thr	Asp	
216		85					90					95					
217																	
218		TAC															436
219		Tyr	Arg	Gln	Ala		Phe	Asp	Arg	Ala		Val	Gly	Trp	Phe		
220	100					105					110					115	
221																	
222		TGG															484
223	Pro	\mathtt{Trp}	Gly	Gln	.	Thr	Leu	۷al	Thr		Ser	Ser	Ala	Ser		Lys	
224					120					125					130		
225																	
226		CCA															532
227	Gly	Pro	Ser		Phe	Pro	Leu	Ala		Ser	Ser	Lys	Ser		Ser	Gly	
228				135					140					145			
229																	
230		ACA															580
231	Gly	Thr		Ala	Leu	Gly	Сув		Val	Lys	qaA	Tyr		Pro	Glu	Pro	
232			150					155					160				
233																	
234		ACG												_			628
235	Val	Thr	Val	Ser	Trp	Asn		GIĀ	Ala	Leu	Thr		GIY	Val	His	Thr	
236		165					170					175					
237			~~~										~-~			ama.	c= c
238		CCG															676
239		Pro	АТа	Val	ьеп		ser	ser	GIĀ	ьeu		ser	Leu	ser	ser		
240	180					185					190					195	
241	ama	3.00	ama	000	maa	3.00	3.00	mma	000	3.00	G3.G	3.00	ma	3.00	maa	330	724
242		ACC															724
243	val	Thr	var	PIO		ser	ser	ьец	GIA		GIII	THE	TYL	TTG		ABII	
244 245					200					205					210		
245	ama.	AAT	CAC	220	ccc	N.C.C	224	N CC	3 3 C	CTC	CAC	220	***	CTT	GNG	CCC	772
																	,,2
247 248	val	Asn	UIS	215	PIO	Ser	ABII	1111	220	Val	veb	пув	пур	225	GIU	PIO	
249				213					220					223			
250	222	TCT	ጥረም	GAC	222	а Ст	CAC	A C A	TGC	CCA	cca	TCC	CCA	CCA	ССТ	GAA	820
251		Ser														_	020
252	шув	per	230	veħ	пур	T 111	1110	235	Cyb	110	110	Cys	240	niu		51 4	
253			230										~ 10				
254	רידירי	CTG	GGG	GGZ	CCG	тсъ	GTC	ጥጥ ር	СТС	ጥጥር	כככ	CCA	444	CCC	AAG	GAC	868
255		Leu															
256	u	245	y	1	0		250					255	_, 5		_, .		
257		~ 1 3					230										
258	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	916
259		Leu															
260	260				~~-	265					270	-10				275	
											_, _					-· ·	

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261																	
262																C GGC	964
263	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	
264					280					285					290		
265																	
266		GAG															1012
267	Val	Glu	Val		Asn	Ala	Lys	Thr		Pro	Arg	Glu	Glu	Gln	Tyr	Asn	
268	,			295					300					305			
269																	
270		ACG															1060
271	Ser	Thr		Arg	Val	Val	Ser		Leu	Thr	Val	Leu		GIn	Asp	Trp	
272			310					315					320				
273 274	CTC	3 3 TT	aca	224	ara.	TT A CT	220	maa	220	ama.	TICC.	220	222	000	OTT C	aas	1100
275		AAT															1108
276	nea	Asn 325	GIŞ	пåв	GIU	ıyı	330	Сув	пЛя	vaı	ser		пåя	ATG	nea	PIO	
277		343					330					335					
278	acc	CCC	አጥሮ	GAG	***	»CC	አጥሮ	TCC	222	ccc	222	aca	CAG	ccc	CGA	CAA	1156
279		Pro															1130
280	340	110	110	GLU	ny 6	345	116	Der	цyо	AIG	350	GLY	GIII		AL 9	355	
281	J.0					3.3					550					333	
282	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG	ACC	AAG	AAC	1204
283		Gln															
284				-1-	360					365					370		
285																	
286	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC	ATC	1252
287	Gln	Val	Ser	Leu	Thr	Сув	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	
288				375		_			380	_		_		385	_		
289																	
290	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	1300
291	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	
292			390					395					400				
293											•						
294		CCT															1348
295	Thr	Pro	Pro	Val	Leu	Asp		Asp	Gly	Ser	Phe		Leu	Tyr	Ser	Lys	
296		405					410					415					
297																	
298		ACC															1396
299		Thr	Val	Asp	_		_	Trp			_		Val	Phe	Ser	Cys	
300	420					425					430					435	
301	maa	ama.	3 m/a	C M	~	aam	ama.	a. a	330	a. a	ma a	3.00	a a	330	300	CITIC .	1444
302																CTC	1444
303 304	ser	Val	met	nis	440	ATG	reg	n18	ABN	H18	TAL	Inr	GIN	пĀв	Ser	теп	
305					440					443					450		
305	TCC	CTG	тст	CCG	CCT	222	ጥር ኔ ረ	<u> </u>	מאכי ל	במרכי	מכר» י	אם כי	יייייי	<u> ፲</u> ርጥር (~		1492
307		Leu					1 GA	- 1 GC(JAC (JGCFM	-G C(-		7476
307	Der	Leu	DGT	455	CTY	-10											
309																	
310	CCG	GCT	CTC (GCGG'	rcgcz	AC G	AGGA'	rgcT:	r GG	CACG	TACC	CCG	rgta(CAT A	ACTTO	CCCGGG	1552
311			'													·	-
312	CGC	CCAG	CAT (ggaai	ATAA	AG C	ACCCI	AGCG	TG	CCT	3GGC	CCC	rgcgz	AAA 2	AAAA	AAAAA	1612

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313																	
314	AAA																1617
315	(2)) IN	FORM	ATIO	N FO	R SE	QID	NO:	10:								
316																	
317			(i)	SEQU													
318) LEI					acid	8						
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322		(:	11) /	MOLE	COLE	TYP	s: p:	rote	ın								
323 324				C 13/0171		DEG	40 T D	T-037	. 05	. TD	NO - 1	10.					
325		(:	K1 <i>)</i> ;	SEQUI	ENCE	ומשת	CRIP	LION	: SE	מד ב	NO:	ro:					
325	Mat	N an	Twn	Thr	Trn	7~~	Pho	Lou	Pho	17-1	17-1	21-	21-	21-	Th-	G1	
327	-19	Asp	пр	1111	-15	Arg	FIIE	пеп	FIIE	-10	Val	AIA	ATG	ALA	-5	GIY	
327	-19				-13					-10					-5		
329	37-1	al n	g.~~	Gln	Wo.+	Gln.	17-1	W-1	61 5	G.~	g1	21-	a 1	17 n 1	Tara	Tara	
330	Val	GIII	Ser	1	Mec	GIII	Val	5	GIII	Ser	GIY	ALG	10	Val	пур	цув	
331				_				J					10				
332	Pro	Glv	Ser	Ser	₩a1	Thr	17a 1	Ser	Cva	Taza	λla	Sar	Glv	Gl v	Thr	Dha	
333	110	15	Der	Der	V 44.1		20	Der	Cyb	מעם	AIG	25	GLY	GLY		1116	
334																	
335	Ser	Asn	Tvr	Ala	Ile	Ser	Tro	Val	Ara	Gln	Ala	Pro	Glv	Gln	Glv	Leu	
336	30		-1-			35			5		40		4 -1	V	4-1	45	
337																	
338	Glu	Trp	Met	Gly	Gly	Ile	Ile	Pro	Leu	Phe	Gly	Thr	Pro	Thr	Tyr	Ser	
339		_		•	50					55	•				60		
340																	
341	Gln	Asn	Phe	Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	
342				65	-	•			70			_	_	75			
343																	
344	Thr	Ala	His	Met	Glu	Leu	Thr	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
345			80					85					90				
346																	
347	Tyr	Tyr	Cys	Ala	Thr	Asp	Arg	Tyr	Arg	Gln	Ala	Asn	Phe	Asp	Arg	Ala	
348		95					100					105					
349																	
350	Arg	Val	Gly	\mathtt{Trp}	Phe	Asp	Pro	\mathtt{Trp}	Gly	Gln	Gly	Thr	Leu	Val	Thr		
351	110					115					120					125	
352														_			
353	Ser	Ser	Ala	Ser		Lys	Gly	Pro	Ser		Phe	Pro	Leu	Ala		Ser	
354					130					135					140		
355	_	_	_		_						_		_	_		_	
356	Ser	Lys	Ser	Thr	Ser	GLY	Gly	Thr		Ala	Leu	GŢĀ	Cys		Val	Lys	
357				145					150					155			
358	•		D1	D	~ 1	D	77 7	m7	777	0	m	3	a	~ 1	27-	7	
359	Asp	туr		Pro	GIU	Pro	vaı		vaı	ser	Trp	ASN		GΤÃ	ATS	теп	
360			160					165					170				
361 362	Th~	g.~	<u></u>	Val	ui.	T L ~	Dha	D~~	71 -	₹7÷1	Loss	61 ~	ge~	ge-	61.	Len	
362 363	Inr	175	GTĀ	val	UIR	III	180	FIO	VIG	val	neu	185	Ser	SAT	GTÅ	TAU	
364		1,3					-00					100					
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365 366 367	Tyr 190	Ser	Leu	Ser	Ser	Val 195	Val	Thr	Val	Pro	Ser 200	Ser	Ser	Leu	Gly	Thr 205
368 369 370	Glı	n Thi	г Ту	r Ile	Э Су: 210	s Ası	n Val	l Ası	n Hi	в Ly: 215	s Pro	o Se:	r Ası	n Th	r Ly: 220	s Val
371 372 373	Asp	Lys	Lys	Val 225	Glu	Pro	Lys	Ser	Сув 230	Asp	Lys	Thr	His	Thr 235	Сув	Pro
374 375 376	Pro	Сув	Pro 240	Ala	Pro	Glu	Leu	Leu 245	Gly	Gly	Pro	Ser	Val 250	Phe	Leu	Phe
377 378 379	Pro	Pro 255	Lys	Pro	Lys	Asp	Thr 260	Leu	Met	Ile	Ser	Arg 265	Thr	Pro	Glu	Val
380 381 382	270	_	Val			275					280				-	285
383 384 385		_	Tyr		290	-				295			•		300	
386 387 388			Glu	305	_				310					315		
389 390 391			His 320		_	_		325				_	330	_	_	
392 393 394		335	Lys				340				-	345			-	
395 396 397	350	-	Gln		_	355				-	360					365
398 399 400	_		Leu		370					375		-			380	_
401 402 403		_	Pro	385	_				390	_				395		
404 405 406			Asn 400	-	-			405				-	410	_	_	
407 408 409		415	Leu	-		-	420			_	-	425				
410 411 412	430		Val			435					440		Leu	His	Asn	His 445
413 414 415 416	Tyr	Thr	Gln	Lys	Ser 450	Leu	Ser	Leu	Ser	Pro 455	Gly	Lys				

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417	(2) I	NFORM	ATIO	N FO	R SE	Q ID	NO:	11:								
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419	(i) SE														
420			A) L				•	-	3							
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425	(1	i) MO	LECU.	LE T	YPE:	CDN	A.									
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427 428	(11	i) HY	POTH	ETIC	AL: I	NO										
429	/.2	-1 337	m	- W												
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433	(1	K) FE			Z 133Z .	ana										
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438			B) L			_		cide								
439		,	D / 11	JCAI.	LOIN:	03.	. 133									
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442			B) L					CIGO								
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446	126	-, 52	2021	·			J211	, <u>, , , , , , , , , , , , , , , , , , </u>			•					
447	CAAGAG	CAG	CGCT	מדכפ	ag Da	ימית	TCCA	7 (7)	ልጥር (acc '	TGG (3CT (TTG (ere (CTC	52
448	0.2.00			0100							Trp 1					32
449									-19		p -		-15			
450																
451	CTC AC	CTC	CTC	ACT	CAG	GAC	ACA	GGG	TCC	TGG	GCC		тст	GCC	CTG	100
452											GCC	CAG	101			
453			ьeu	TIIT	GIII	ADU	Thr	Glv	Ser							
45.		-10		1111	GIN	App	Thr	Gly	Ser							
454				1111	GIN	veħ		Gly	Ser			Gln				
454 455	ACT CA	-10				_	-5	-		Trp	Ala	Gln 1	Ser	Ala	Leu	148
	ACT CA	-10 3 CCT	GCC	TCC	GTG	TCT	-5 GGG	TCT	CCT	Trp	Ala	Gln 1 TCG	Ser	Ala	Leu	148
455		-10 3 CCT	GCC	TCC	GTG	TCT	-5 GGG	TCT	CCT	Trp	Ala	Gln 1 TCG	Ser	Ala	Leu	148
455 456	Thr Gl	-10 3 CCT	GCC	TCC	GTG Val	TCT	-5 GGG	TCT	CCT	Trp GGA Gly	Ala	Gln 1 TCG	Ser	Ala	Leu ATC Ile	148
455 456 457	Thr Gl	-10 G CCT	GCC Ala	TCC Ser	GTG Val 10	TCT Ser	-5 GGG Gly	TCT Ser	CCT Pro	GGA Gly 15	Ala CAG Gln	Gln 1 TCG Ser	Ser ATC Ile	Ala ACC Thr	ATC Ile 20	148
455 456 457 458	Thr Gl	-10 G CCT n Pro	GCC Ala GGA	TCC Ser	GTG Val 10	TCT Ser	-5 GGG Gly GAT	TCT Ser	CCT Pro	GGA Gly 15	Ala CAG Gln TAT	Gln 1 TCG Ser	Ser ATC Ile	Ala ACC Thr	ATC Ile 20	
455 456 457 458 459	Thr Gl	-10 G CCT n Pro	GCC Ala GGA	TCC Ser	GTG Val 10	TCT Ser	-5 GGG Gly GAT	TCT Ser	CCT Pro	GGA Gly 15	Ala CAG Gln TAT	Gln 1 TCG Ser	Ser ATC Ile	Ala ACC Thr	ATC Ile 20	
455 456 457 458 459 460	Thr Gl	-10 G CCT n Pro	GCC Ala GGA	TCC Ser ACC Thr	GTG Val 10	TCT Ser	-5 GGG Gly GAT	TCT Ser	CCT Pro	GGA Gly 15	Ala CAG Gln TAT	Gln 1 TCG Ser	Ser ATC Ile	Ala ACC Thr GTC Val	ATC Ile 20	
455 456 457 458 459 460 461	Thr Gl	-10 G CCT n Pro C ACT s Thr	GCC Ala GGA Gly	TCC Ser ACC Thr 25	GTG Val 10 AAC Asn	TCT Ser AAT Asn	-5 GGG Gly GAT Asp	TCT Ser GTT Val	CCT Pro GGG Gly 30	GGA Gly 15 AGT Ser	Ala CAG Gln TAT Tyr	Gln 1 TCG Ser AAC Asn	ATC Ile CTT Leu	Ala ACC Thr GTC Val 35	ATC Ile 20	
455 456 457 458 459 460 461 462	Thr Gl	-10 G CCT n Pro C ACT s Thr	GCC Ala GGA Gly	TCC Ser ACC Thr 25	GTG Val 10 AAC Asn	TCT Ser AAT Asn	-5 GGG Gly GAT Asp	TCT Ser GTT Val	CCT Pro GGG Gly 30	GGA Gly 15 AGT Ser	Ala CAG Gln TAT Tyr	Gln 1 TCG Ser AAC Asn	ATC Ile CTT Leu ATT	Ala ACC Thr GTC Val 35	ATC Ile 20 TCC Ser	196
455 456 457 458 459 460 461 462 463	Thr Gl. 5 TCC TG Ser Cy TGG TA	-10 G CCT n Pro C ACT s Thr	GCC Ala GGA Gly	TCC Ser ACC Thr 25	GTG Val 10 AAC Asn	TCT Ser AAT Asn	-5 GGG Gly GAT Asp	TCT Ser GTT Val	CCT Pro GGG Gly 30	GGA Gly 15 AGT Ser	Ala CAG Gln TAT Tyr	Gln 1 TCG Ser AAC Asn	ATC Ile CTT Leu ATT	Ala ACC Thr GTC Val 35	ATC Ile 20 TCC Ser	196
455 456 457 458 459 460 461 462 463 464	Thr Gl. 5 TCC TG Ser Cy TGG TA	-10 G CCT n Pro C ACT s Thr	GCC Ala GGA Gly CAG Gln	TCC Ser ACC Thr 25	GTG Val 10 AAC Asn	TCT Ser AAT Asn	-5 GGG Gly GAT Asp	TCT Ser GTT Val	CCT Pro GGG Gly 30	GGA Gly 15 AGT Ser	Ala CAG Gln TAT Tyr	Gln 1 TCG Ser AAC Asn	ATC Ile CTT Leu ATT Ile	Ala ACC Thr GTC Val 35	ATC Ile 20 TCC Ser	196
455 456 457 458 459 460 461 462 463 464 465	Thr Gl. 5 TCC TG Ser Cy TGG TA	-10 G CCT n Pro C ACT s Thr C CAG	GCC Ala GGA Gly CAG Gln 40	TCC Ser ACC Thr 25 CAC His	GTG Val 10 AAC Asn CCA Pro	TCT Ser AAT Asn GGC Gly	-5 GGG Gly GAT Asp AAA Lys	TCT Ser GTT Val GCC Ala 45	CCT Pro GGG Gly 30 CCC Pro	GGA Gly 15 AGT Ser AAA Lys	Ala CAG Gln TAT Tyr ATC Ile	Gln 1 TCG Ser AAC Asn ATG Met	ATC Ile CTT Leu ATT Ile 50	Ala ACC Thr GTC Val 35 TAT Tyr	ATC Ile 20 TCC Ser	196
455 456 457 458 459 460 461 462 463 464 465 466	Thr Gl. 5 TCC TG Ser Cy TGG TA Trp Ty	-10 G CCT n Pro C ACT s Thr C CAG r Gln	GCC Ala GGA Gly CAG Gln 40	TCC Ser ACC Thr 25 CAC His	GTG Val 10 AAC Asn CCA Pro	TCT Ser AAT Asn GGC Gly	-5 GGG Gly GAT Asp AAA Lys	TCT Ser GTT Val GCC Ala 45	CCT Pro GGG Gly 30 CCC Pro	GGA Gly 15 AGT Ser AAA Lys	Ala CAG Gln TAT Tyr ATC Ile	Gln 1 TCG Ser AAC Asn ATG Met	ATC Ile CTT Leu ATT Ile 50 GGC	Ala ACC Thr GTC Val 35 TAT Tyr	ATC Ile 20 TCC Ser GAG Glu	196 244

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469			55					60					65				
470																	
471															GAG		340
472 473	ser	-	ASN	Thr	ATA	ser		Thr	тте	ser	GIY		GIN	ATA	Glu	Asp	
474		70					75					80					
475	GAG	ССТ	СУТ	тат	TAC	тсс	тсс	тса	тат	CCA	ССТ	ልርጥ	TAC	ልሮሞ	GTG	CTT	388
476															Val		300
477	85			-,-	-1-	90	U , D		-1-		95		-1-		***	100	
478	•										-						
479	TTC	GGC	GGA	GGG	ACC	AAA	CTG	ACC	GTC	CTA	GGT	CAG	CCC	AAG	GCT	GCC	436
480	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala	Ala	
481		_	_	_	105	_				110	_			_	115		
482																	
483	CCC	TCG	GTC	ACT	CTG	TTC	CCG	CCC	TCC	TCT	GAG	GAG	CTT	CAA	GCC	AAC	484
484	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu	Glu	Leu	Gln	Ala	Asn	
485				120					125					130			
486																	
487															GCC		532
488	Lys	Ala		Leu	Val	Сув	Leu		Ser	Asp	Phe	Tyr		Gly	Ala	Val	
489			135					140					145				
490						~~~	~~ m			~~~	ama		-	aa .	ama	63.6	E00
491 492															GTG		580
493	III	150	AId	пр	гуя	ATA	155	Ser	ser	PIO	vai	160	ALG	GTĀ	Val	GIU	
494		130					133					100					
495	ACC	ACC	ACA	CCC	TCC	AAA	CAA	AGC	AAC	AAC	AAG	TAC	GCG	GCC	AGC	AGC	628
496															Ser		
497	165					170					175	-2-				180	
498																	
499	TAT	CTG	AGC	CTG	ACG	CCT	GAG	CAG	TGG	AAG	TCC	CAC	AGA	AGC	TAC	AGC	676
500	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser	His	Arg	Ser	Tyr	Ser	
501					185					190					195		
502																	
503															GCC		724
504	Cys	Gln	Val		His	Glu	Gly	Ser		Val	Glu	Lys	Thr		Ala	Pro	
505				200					205					210			
506																	
507				TCA	TAG	STTC:	raa A	ACCC:	rcac	cc co	CCCC	ACGG	3 AG	ACTA(JAGC		776
508	Thr	GIU	Сув	ser													
509 510			215														
511	TCC:	א כבאי	דיכים נ	73.00	ca co	בם פי	րტოტ	יירירייי	י ככי	مححد	ממר	GCA'	ר מ מ מים	מרר (מייים מייים	CCCTG	836
512	160	AGGA.		CAGG	JGAG	3G G.	LCIC.			accc.	JARG	GCA.	ı Cırı	300			050
513	CAC	rcaa'	raa 2	ACCC'	rcaa'	ra a	ATAT	CTC	A TTO	STCA	ATCA	CAA	AAAA	AAA 2	AAAA	AAAAA	896
514									,								
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518	(2)	INI	FORM	ATIO	N FO	R SE	Q ID	NO:	12:								
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Patent Application US/07/952,640

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-19				-15					-10					-5				
Ser	Trp	Ala	Gln	Ser	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser			
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Pro	Glv	Gln	Ser	Tle	Thr	Tle	Ser	Cvs	Thr	Glv	Thr	Agn	Agn	Asn	Val			
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Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Сув	Cys	Ser	Tyr			
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Ala	Gly	Ser	Tyr	Thr	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val			
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_			_							_	_		_	_	_			
Asp	Phe	Tyr		Gly	Ala	Val	Thr		Ala	Trp	Lys	Ala		Ser	ser			
			145					150					155					
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Pro	Val	_	Ala	Gly	Val	Glu		Thr	Thr	Pro	Ser		Gln	Ser	Asn			
		160					165					170						
Asn	Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp			
	175	-				180	-				185				-			
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	-19 Ser Pro Gly 30 Pro Asn Leu 110 Ser Asp Pro Asn	Met Ala- 19 Trp Ser Trp Pro Gly 15 Gly Ser 30 Eys Asn Arg Ser Gly Ala Gly 110 Gly 110 Gly 110 Fro Val Asp Phe Pro Val Asn Lys 175 Lys Ser	Met Ala Trp -19 Ser Trp Ala Pro Gly Gln 15 Gly Ser Tyr 30 Pro Lys Ile Asn Arg Phe Ser Gly Leu 80 Ala Gly Ser 95 Leu Gly Gln 110 Ser Glu Glu Asp Phe Tyr Pro Val Lys 160 Asn Lys Tyr 175 Lys Ser His	(xi) SEQUIO Met Ala Trp Ala Ser Trp Ala Gln Pro Gly Gln Ser Asn Arg Phe Ser Ser Gly Leu Gln Ala Gly Ser Tyr Leu Gly Ser Tyr Leu Gly Gln Pro Asp Phe Tyr Pro Asp Phe Tyr Ala Lys Tyr Ala Lys Ser His Arg	(xi) SEQUENCE Met 19 Ala Trp Ala Leu 15 Ser Trp Ala Gln Ser 11 Ser 11 Pro Gly Gln Ser Ile 15 Leu Asn Leu 15 Pro Lys Ile Met Ile 50 Asn Arg Phe Ser Gly 65 Ser Gly Leu Gln Ala 80 Ala 81 Ala Gly Ser Tyr Thr 95 Tyr Thr 130 Leu Gly Gln Pro Lys 110 Ser Gly Leu Gln 130 Asp Phe Tyr Pro Gly 145 Gly 145 Pro Val Lys Ala Gly 160 Ala Gly Ala Ser 175 Lys Ser His Arg Ser	(xi) SEQUENCE DESCRIPTION Met Ala Trp Ala Leu Leu -15 Leu -15 Ser Trp Ala Gln Ser Ala 1 Ser Ala 1 Pro Gly Gln Ser Ile Thr 15 Tyr Asn Leu Val 35 Pro Lys Ile Met Ile Tyr 50 Tyr Ser Gly Ser Gly Ser 65 Ser Gly Leu Gln Ala Glu 80 Ala Glu Ala Glu Ala 115 Leu Gly Gln Pro Lys Ala 115 Ser Glu Glu Leu Gln Ala 115 Ser Glu Glu Leu Gln Ala 130 Ala 130 Asp Phe Tyr Pro Gly Ala 145 Pro Val Lys Ala Gly Val 160 Asn Lys Tyr Ala Ala Ser 175 Tyr Ala Ala Ser 175 Lys Ser His Arg Ser Tyr	(xi) SEQUENCE DESCRIPT Met Ala Trp Ala Leu Leu Leu Ser Trp Ala Gln Ser Ala Leu Pro Gly Gln Ser Ile Tyr Asn Leu Val Ser Pro Lys Ile Met Ile Tyr Glu Asp Asn Arg Phe Ser Gly Ser Lys Ala Gly Ser Tyr Thr Val Val Ser Gly Gln Pro Lys Ala Ala Leu Gly Gln Pro Lys Ala Ala Ser Glu Leu Gln Ala Ala Ala Asp Phe Tyr Pro Gly Ala Val Asp Phe Tyr Pro Gly Ala Val Asp Lys Tyr Ala Ala Ser Ser Lys Ser	(xi) SEQUENCE DESCRIPTION Met Ala Trp Ala Leu Leu Leu Leu -19 Ala Cln Ser Ala Leu Thr 5 Ser Trp Ala Gln Ser Ile Thr Ile Ser 15 Ser Tyr Asn Leu Val Ser Trp 30 Pro Lys Ile Met Ile Tyr Glu Val 50 Ser Gly Ser Lys Ser 65 Ser Gly Leu Gln Ala Glu Asp Glu 85 Ala Gly Ser Tyr Thr Val Val Phe 100 Leu Gly Gln Pro Lys Ala Ala Pro 110 Ser Glu Glu Leu Gln Ala Asn Lys 130 Asp Phe Tyr Pro Gly Ala Val Thr 145 Pro Val Lys Ala Gly Val Glu Thr 165 Asn Lys Tyr Ala Ala Ser Ser Ser Tyr 180 Lys Ser His Arg Ser Tyr Ser Cys	Met -19 Ala Trp Ala Leu -15 Leu Leu Leu Thr S Cln Ser Trp Ala Gln Ser Ala Leu Thr S Cln Pro Gly Gln Ser Jue Thr Jue Ser S Trp Tyr 30 Ser Tyr Asn Leu Yal Ser Trp Tyr Pro Lys Jue Ser Ser Gly Ser Lys Ser Gly 70 Asn Arg Phe Ser Gly Ser Lys Ser Gly 70 Ser Gly Leu Gln Ala Glu Asp Ser Ry Ala Gly Ser Tyr Thr Val 100 Phe Gly 115 Leu Gly Ser Tyr Thr Val 100 Phe Gly 115 Ser Glu Glu Leu Gln Ala Ala Pro Ser 115 Ser Glu Glu Leu Gln Ala Asn Lys Ala Asp Phe Tyr Pro Gly Ala Val Thr Val 150 Pro Val Lys Ala Gly Val Glu Thr Thr 150 Asn Lys Tyr Ala Ala Ser Ser Ser Tyr Leu 180 Lys Ser His Arg Ser Tyr Ser Cys Gln	(xi) SEQUENCE DESCRIPTION: SEQ ID Met Ala Trp Ala Leu Leu Leu Thr Leu Ser Trp Ala Gln Ser Ala Leu Thr Gln Pro Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Asn Leu Val Ser Trp Tyr Gln Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Ala Gly Ser Tyr Thr Val Val Phe Gly Gly Leu Gly Ala Ala Ala Arg Phe Gly Ala Asp Phe Tyr Pro Gly Ala Asn Lys Ala Thr Asp Phe Tyr Pro Gly Ala Val <t< td=""><td>(xi) SEQUENCE DESCRIPTION: SEQ ID Not: Met Ala Trp Ala Leu Leu Leu Thr Leu Leu Leu Thr Leu Leu Leu Thr Leu Leu Thr Leu Leu Thr Leu Thr Leu Thr Leu Thr Leu Thr Thr Leu Thr Thr Thr Gly Ser Thr Gly Ang A</td><td>(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr -10 Leu Thr -10 Leu Thr -10 Leu Thr Leu Leu Thr Leu Leu Thr -10 Leu Thr -10 Ser Thr -10 Ala Ser Ala Ala Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala</td><td> (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln -19</td><td>(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Ala Trp Ala Leu Leu Leu Thr Leu Thr Leu Thr Gln Pro Ala Ser Val Ser Leu Thr Asn Leu Thr Lu Ser Cys Thr Gly Thr Asn Asn Asn Asn Leu Val Ser Thr Gly Thr Asn Thr Lu Asn Lu Asn Thr Lu Asn Lu Asn Thr</td><td> (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Asp Thr -19</td><td>(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Asp Thr Gly -15 Trp Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Trp Ala Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Asn Asn Asn Asp Val 15 Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gln Gln His Pro Gly Lys Ala 30 Ser Tyr Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala 45 Pro Lys Ile Met Ile Tyr Glu Val Ser Lys Arg Pro Ser Gly Val Ser 60 Ser Gly Leu Thr Ile 75 Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile 75 Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr 90 Ala Gly Ser Tyr Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val 100 Ser Glu Glu Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser 125 Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser 130 Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser 140 Asp Phe Tyr Pro Ala Ala Glu Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn 160 Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp 175 Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr</td><td>Met Ala Trp Ala Leu Leu Leu Leu Leu Thr -19 See Ala Leu Leu Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Trp Ala Gln Ser Ala Leu Thr Je Ser Cys Thr Gly Thr Asn Asn Asn Asp Val 15 Ser Trp Ala Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Asn Asn Asn Asp Val 15 Gly Ser Tyr Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala 30 Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile 70 Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile 75 Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr 80 Ala Gly Ser Tyr Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val 100 Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser 115 Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser 130 Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser 145 Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn 160 Asp Lys Tyr Ala Ala Ser Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr</td><td>Met Ala Trp Ala Leu Leu Leu Leu Leu Thr Clu Leu Thr Gln Asp Thr Gly -19 Ala Leu Leu Leu Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Trp Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser 10 Ser Trp Ala Gln Ser Ala Leu Thr Ile Ser Cys Thr Gly Thr Asn Asn Asp Val 15 Ser Trp Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala 30 Gly Ser Tyr Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala 30 Asn Asp Pro Ser Gly Lys Asp Pro Ser Gly Val Ser Lys Asp Pro Ser Gly Val Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile 70 Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile 65 Asn Tyr Tyr Tyr Cys Cys Ser Tyr 90 Ala Gly Ser Tyr Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val 100 105 Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser 125 125 Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser 130 135 Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser 140 155 Pro Val Lys Ala Gly Val Glu Thr Thr Thr Thr Pro Ser Lys Gln Ser Asn 160 160 Asn Lys Tyr Ala Ala Ser Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr</td></t<>	(xi) SEQUENCE DESCRIPTION: SEQ ID Not: Met Ala Trp Ala Leu Leu Leu Thr Leu Leu Leu Thr Leu Leu Leu Thr Leu Leu Thr Leu Leu Thr Leu Thr Leu Thr Leu Thr Leu Thr Thr Leu Thr Thr Thr Gly Ser Thr Gly Ang A	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr -10 Leu Thr -10 Leu Thr -10 Leu Thr Leu Leu Thr Leu Leu Thr -10 Leu Thr -10 Ser Thr -10 Ala Ser Ala Ala Ala Ser Ala	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln -19	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Ala Trp Ala Leu Leu Leu Thr Leu Thr Leu Thr Gln Pro Ala Ser Val Ser Leu Thr Asn Leu Thr Lu Ser Cys Thr Gly Thr Asn Asn Asn Asn Leu Val Ser Thr Gly Thr Asn Thr Lu Asn Lu Asn Thr Lu Asn Lu Asn Thr	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Asp Thr -19	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Asp Thr Gly -15 Trp Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Trp Ala Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Asn Asn Asn Asp Val 15 Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gln Gln His Pro Gly Lys Ala 30 Ser Tyr Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala 45 Pro Lys Ile Met Ile Tyr Glu Val Ser Lys Arg Pro Ser Gly Val Ser 60 Ser Gly Leu Thr Ile 75 Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile 75 Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr 90 Ala Gly Ser Tyr Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val 100 Ser Glu Glu Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser 125 Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser 130 Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser 140 Asp Phe Tyr Pro Ala Ala Glu Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn 160 Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp 175 Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr	Met Ala Trp Ala Leu Leu Leu Leu Leu Thr -19 See Ala Leu Leu Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Trp Ala Gln Ser Ala Leu Thr Je Ser Cys Thr Gly Thr Asn Asn Asn Asp Val 15 Ser Trp Ala Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Asn Asn Asn Asp Val 15 Gly Ser Tyr Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala 30 Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile 70 Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile 75 Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr 80 Ala Gly Ser Tyr Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val 100 Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser 115 Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser 130 Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser 145 Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn 160 Asp Lys Tyr Ala Ala Ser Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr	Met Ala Trp Ala Leu Leu Leu Leu Leu Thr Clu Leu Thr Gln Asp Thr Gly -19 Ala Leu Leu Leu Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Trp Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser 10 Ser Trp Ala Gln Ser Ala Leu Thr Ile Ser Cys Thr Gly Thr Asn Asn Asp Val 15 Ser Trp Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala 30 Gly Ser Tyr Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala 30 Asn Asp Pro Ser Gly Lys Asp Pro Ser Gly Val Ser Lys Asp Pro Ser Gly Val Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile 70 Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile 65 Asn Tyr Tyr Tyr Cys Cys Ser Tyr 90 Ala Gly Ser Tyr Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val 100 105 Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser 125 125 Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser 130 135 Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser 140 155 Pro Val Lys Ala Gly Val Glu Thr Thr Thr Thr Pro Ser Lys Gln Ser Asn 160 160 Asn Lys Tyr Ala Ala Ser Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr

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Raw Sequence Listing

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573 574 575 576 577 578		(i)	() () ()	QUENCA) LIB) TO	engti Ype : [rani	H: 32 nuc: DEDNI	21 ba leic ESS:	ase p acid bot	pair: d	5							
579 580		(ii)	MOI	LECUI	LE T	YPE:	cDN	A.									
581 582	•	(iii)	HY)	РОТНІ	ETIC	AL: 1	.TO										
583																	
584 585 586		(iv)) AN	ri-Si	ense	: NO											
587		(ix)) FE	ATURI	⊑:												
588			-	A) N2	•												
589			(1	B) L(CAT:	ION:	1	321									
590 591																	
592		(xi)) SE	OUEN	CE DI	ESCR:	IPTI	ON:	SEQ :	ID NO	0:13	:					
593		• • • • • • • • • • • • • • • • • • • •							_								
594	GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTA	GGA	48
595	Asp	Ile	Gln	Met		Gln	Ser	Pro	Ser		Leu	Ser	Ala	Ser		Gly	
596	1				5					10					15		
597	a. a		ama.				maa	a aa	<i>a</i> as	3 CM	a. a	3.00	3 mm			m = m	0.6
598		AGA															96
599 600	Авр	Arg	vai	20	TIE	Thr	Сув	Arg	A1a 25	ser	GIN	ser	TIE	30	ABII	TYP	
601				20					43					30			
602	TTA	AAT	TGG	TAT	CAA	CAG	AAA	CCA	GGG	AAA	GCC	CCT	AAG	CTC	CTG	ATC	144
603		Asn															
604			35	•				40	•	•			45				
605																	
606	TAT	GCT	GCA	TCC	AGT	TTG	CAA	AGT	GGG	GTC	ACA	TCA	AGG	TTC	AGT	GGC	192
607	Tyr	Ala	Ala	Ser	Ser	Leu		Ser	Gly	Val	Thr		Arg	Phe	Ser	Gly	
608		50					55					60					
609									~-~					~~~	~~~		240
610 611		GGA Gly															240
612		GIY	ser	GTĀ	THE	70	FIIG	1111	пеп	1111	75	Ser	ser	Tea	GIII	80	
613	0.5					, 0					, 5					00	
614	GAA	GAT	TCT	GCA	ACT	TAC	TAC	TGT	CAA	CAG	AGT	TAC	AGT	ACC	CTG	ATC	288
615		Asp															
616		_			85	_	_	_		90		_			95		
617																	
618		TTC															321
619	Thr	Phe	Gly		Gly	Thr	Arg	Leu		Ile	Lys						•
620				100					105								
621 622																	
623	12) INI	rorm:	י∩דיים	יחיד ע	R STO	חד כ	NO •	14 •								
624	, 4	,			01			_,_,	•								

Raw Sequence Listing

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625			(i)	SEQU	ENCE	CHA	RACT	ERIS'	rics	:						
626				(A)) LE	NGTH	: 10	7 am:	ino a	acid	3					
627				(B)	TY:	PE: a	amino	ac:	id							
628				(D)	TO:	POLO	GY: :	line	ar							
629																
630		(:	ii) 1	MOLE	CULE	TYP	E: p:	rote	in							
631							_									
632		(:	xi) :	SEQUI	ENCE	DES	CRIP:	rion	: SE	Q ID	NO:	14:				
633										-						
634	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
635	ī				5					10					15	_
636																
637	Asp	Arg	Val	Thr	Ile	Thr	Сув	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Asn	Туз
638				20				_	25					30		_
639																
640	Leú	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
641			35	_			_	40	_	-			45			
642																
643	Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Thr	Ser	Arg	Phe	Ser	Gly
644	_	50					55		_			60	_			_
645																
646	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
647	65	_		_		70					75					80
648																
649	Glu	Asp	Ser	Ala	Thr	Tyr	Tyr	Сув	Gln	Gln	Ser	Tyr	Ser	Thr	Leu	Ile
650					85					90					95	
651																
652	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys					
653				100					105							
654																
655	(2)	IN	FORM	ATIO	N FO	R SE	Q ID	NO:	15:							
656																
657		(i)) SE	QUEN	CE CI	HARA	CTER:	ESTI	CS:							
658			()	A) LI	ENGT	H: 32	24 ba	ase p	pairs	3		·				
659			(1	B) T	PE:	nuc.	leic	acio	£							
660			((C) Si	rani	DEDNI	ESS:	botl	n							
661			(1	D) T	OPOL	OGY:	line	ear					•			
662																
663		(ii)) MO	LECUI	LE T	YPE:	CDN	A								
664																
665		(iii)) HY	POTH	ETIC	AL: 1	OV									
666																
667		(iv)	AN:	TI-SI	ense	: NO										
668																
669																
670		(ix)		ATURI												
671			(2	A) N	AME/I	KEY:	CDS									
672			(1	B) L	CAT:	ON:	13	324								
673																
674																
675		(xi)) SE	QUEN	CE DI	ESCR:	[PTI	ON: S	SEQ :	D NO	:15	:				
676																

Raw Sequence Listing

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677	GAC	ΔТТ	CAG	CTG	» CC	CAG	ጥሮጥ	CCA	ጥረጥ	TOO	CTC	T/CT	CCA	TICC	CITTA	aa.		8
678				Leu													3	. 0
679	1				5					10					15	3		
680																		
681				ACC													9	6
682 683	Asp	Arg	Val	Thr	Ile	Thr	Сув	Arg		Ser	Gln	Gly	Ile		Asp	Tyr		
684				20					25					30				
685	TTA	AGT	TGG	TAT	CAG	CAG	AAA	CCA	GGG	222	GCC	ССТ	GAG	CTC	СТС	ATC	14	.4
686				Tyr														•
687			35	•			•	40	•	•			45					
688																		
689	TAT	GCT	GCT	TCC	AGT	TTG	CAA	AGT	GGG	ATT	CCC	TCT	CGG	TTC	AGC	GGC	19	2
690	Tyr		Ala	Ser	Ser	Leu		Ser	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Gly		
691		50					55					60						
692 693	» Cim	CCA	mam	000	3.03	C a m	mma	3 CIM	ama	3.00	3 ma	3.00	3.00	ama	~~~	aam.	0.4	_
694				GGG Gly													24	U
695	65	GLY	Der	GLY	1111	70	1110	1111	пец	T11.L	75	Der	Der	пец	GIII	80		
696																		
697	GAA	GAT	TCT	GCA	GTT	TAT	TAC	TGT	CAA	CAC	ACT	TAT	AGT	GAC	CCG	TAC	28	8
698	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Сув	Gln	His	Thr	Tyr	Ser	Asp	Pro	Tyr		
699					85					90					95			
700																		
701 702				CAG						_							32	4
702	ser	Pne	GIY	Gln 100	GIÃ	THE	гув	val	105	TTE	гув	Arg						
704				100					103									
705	•																	
706	(2)	T 3.71			T POI	SEC	ID (NO:	L6:									
	(4)	TMI	PORM	IOLT!	1 POI	,												
707	(2)	TNI	FORM	ATION	· FOI	,	-											
708	(2)			ATION SEQUE		-	- RACTI	RIST	rics:	;								
708 709	(2)			EEQUE	ENCE LEI	CHAI NGTH :	108	am:	ino a		3							
708 709 710	(2)			SEQUI (A) (B)	ENCE LEI	CHAINGTH:	108 mino	ami aci	ino a id		3							
708 709 710 711	(2)			SEQUI (A) (B)	ENCE LEI	CHAI NGTH :	108 mino	ami aci	ino a id		3							
708 709 710 711 712	(2)		(i) £	EEQUE (A) (B) (D)	ENCE LEI TYI	CHAI NGTH: PE: 6	: 108 mino FY:]	ami aci	ino a id ar		3							
708 709 710 711	(2)		(i) £	SEQUI (A) (B)	ENCE LEI TYI	CHAI NGTH: PE: 6	: 108 mino FY:]	ami aci	ino a id ar		3							
708 709 710 711 712 713	(2)	(±	(i) £	EEQUE (A) (B) (D)	ENCE LEI TYI TOI	CHAI NGTH: PE: 6 POLOC	: 108 amino 3Y:] E: pr	ami aci linea	ino a id ar in	acida		L6:						
708 709 710 711 712 713 714	(2)	(±	(i) £	EEQUE (A) (B) (D)	ENCE LEI TYI TOI	CHAI NGTH: PE: 6 POLOC	: 108 amino 3Y:] E: pr	ami aci linea	ino a id ar in	acida		L6:						
708 709 710 711 712 713 714 715 716 717		t) c)	(i)	EEQUE (A) (B) (D)	ENCE LEI TYI TOI CULE	CHAI NGTH: PE: 6 POLOG TYPI DESC	108 mino Y: 1 E: pr	ami aci inea cotei	ino a id ar in : SE(acida	NO: I		Ala	Ser	Val	Gly		
708 709 710 711 712 713 714 715 716 717		t) c)	(i)	GEQUE (A) (B) (D) MOLEC	ENCE LEI TYI TOI CULE	CHAI NGTH: PE: 6 POLOG TYPI DESC	108 mino Y: 1 E: pr	ami aci inea cotei	ino a id ar in : SE(acida	NO: I		Ala	Ser	Val 15	Gly		
708 709 710 711 712 713 714 715 716 717 718 719	Asp 1	(; (; Ile	(i) s ii) h ci) s	GEQUE (A) (B) (D) MOLEC GEQUE Leu	ENCE TYI TOI CULE ENCE Thr	CHAI NGTH: PE: 8 POLOC TYPI DESC	: 108 amino GY:] E: pr CRIPT	ami o aci linea rotei rION:	ino a id in : SE() ID Ser 10	NO: 1	Ser			15	-		
708 709 710 711 712 713 714 715 716 717 718 719 720	Asp 1	(; (; Ile	(i) s ii) h ci) s	SEQUE (A) (B) (D) MOLEC SEQUE Leu	ENCE TYI TOI CULE ENCE Thr	CHAI NGTH: PE: 8 POLOC TYPI DESC	: 108 amino GY:] E: pr CRIPT	ami o aci linea rotei rION:	ino a id in : SEÇ Ser) ID Ser 10	NO: 1	Ser		Ser	15	-		
708 709 710 711 712 713 714 715 716 717 718 719 720 721	Asp 1	(; (; Ile	(i) s ii) h ci) s	GEQUE (A) (B) (D) MOLEC GEQUE Leu	ENCE TYI TOI CULE ENCE Thr	CHAI NGTH: PE: 8 POLOC TYPI DESC	: 108 amino GY:] E: pr CRIPT	ami o aci linea rotei rION:	ino a id in : SE() ID Ser 10	NO: 1	Ser			15	-		
708 709 710 711 712 713 714 715 716 717 718 719 720 721 722	Asp 1	(; () Ile Arg	(i) S ii) B ci) S Gln Val	SEQUE (A) (B) (D) MOLEC SEQUE Leu Thr 20	ENCE TYI TOI CULE ENCE Thr 5	CHAINGTH: PE: 6 POLOG TYPE DESC	: 108 amino E: pr CRIPT Ser	B ami p aci lines rotei rION: Pro Arg	ino aid ar in Ser Ala 25	O ID Ser 10	NO:1 Leu Gln	Ser Gly	Ile	Ser 30	15 Asp	Tyr		
708 709 710 711 712 713 714 715 716 717 718 719 720 721	Asp 1	(; () Ile Arg	(i) S ii) B ci) S Gln Val	SEQUE (A) (B) (D) MOLEC SEQUE Leu	ENCE TYI TOI CULE ENCE Thr 5	CHAINGTH: PE: 6 POLOG TYPE DESC	: 108 amino E: pr CRIPT Ser	B ami p aci lines rotei rION: Pro Arg	ino aid ar in Ser Ala 25	O ID Ser 10	NO:1 Leu Gln	Ser Gly	Ile	Ser 30	15 Asp	Tyr		
708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723	Asp 1	(; () Ile Arg	(i) S ii) N ci) S Gln Val	SEQUE (A) (B) (D) MOLEC SEQUE Leu Thr 20	ENCE TYI TOI CULE ENCE Thr 5	CHAINGTH: PE: 6 POLOG TYPE DESC	: 108 amino E: pr CRIPT Ser	B ami b aci linea rotei rION: Pro Arg	ino aid ar in Ser Ala 25	O ID Ser 10	NO:1 Leu Gln	Ser Gly	Ile Glu	Ser 30	15 Asp	Tyr		
708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726	Asp 1 Asp Leu	(; Ile Arg	(i) S ii) S ci) S Gln Val Trp 35	SEQUE (A) (B) (D) MOLEC SEQUE Leu Thr 20	ENCE TYI TOI CULE ENCE Thr 5	CHAINGTH: PE: 6 POLOG TYPE DESC Gln Thr	: 108 Amino E: pr CRIPT Ser Cys	B ami b aci linea rotei Pro Arg Pro 40	ino aid in : SE(Ser Ala 25	O ID Ser 10 Ser	NO:1 Leu Gln Ala	Ser Gly Pro	Ile Glu 45	Ser 30 Leu	15 Asp Leu	Tyr Ile		
708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725	Asp 1 Asp Leu	(; Ile Arg	(i) S ii) S ci) S Gln Val Trp 35	SEQUE (A) (B) (D) MOLEC SEQUE Leu Thr 20	ENCE TYI TOI CULE ENCE Thr 5	CHAINGTH: PE: 6 POLOG TYPE DESC Gln Thr	: 108 Amino E: pr CRIPT Ser Cys	B ami b aci linea rotei Pro Arg Pro 40	ino aid in : SEG Ser Ala 25	O ID Ser 10 Ser	NO:1 Leu Gln Ala	Ser Gly Pro	Ile Glu 45	Ser 30 Leu	15 Asp Leu	Tyr Ile		

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730 731	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75	Ser	Ser	Leu	Gln	Pro 80	
732 733	Glu	Asp	Ser	Ala	Val 85	Tyr	Tyr	Сув	Gln	His 90	Thr	Tyr	Ser	Asp	Pro 95	Tyr	
734																	
735	Ser	Phe	Gly		Gly	Thr	Lys	Val	_	Ile	Lys	Arg					
736 737				100					105								
738	(2)	TNI	7ORM	TTO	v FOI	SEC) ID	NO:	17:								
739	(2)		· Olum			,	2		-,.								
740		(i)	SE	QUEN	CE CI	IARA	CTER	ISTI	cs:								
741			(2	A) LI	ENGTI	I: 32	24 ba	ase p	pair	3							
742			(1	3) T	YPE:	nucl	leic	acio	£								
743				-			ESS:		a								
744			(1) T(OPOL	OGY:	line	ear									
745		,						_									
746 747		(11)	MOI	-ECUI	PR T.	(PE:	cDN2	A.									
748		(444)	HYI	ועיד∧כ	2TT (*)	\ T. • 1	īO.										
749	,	(,	HII	OIM	31 I Ç	ти: т	NO										
750		(iv)	AN'	CI-SI	ENSE	: NO											
751		(,															
752																	
753		(ix)	FE2	ATURI	3:												
754			(2	A) N2	AME/I	KEY:	CDS										
755			(1	3) L(CAT:	: MOI	13	324									
756																	
757																	
757 758		(xi)	SE(QUENC	CE DI	SCR	[PTIC	ON: S	SEQ :	ED NO):17:	:					
757 758 759	CAC												CCT	m/dm	CT A	CCA	49
757 758 759 760		ATT	CAG	CTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT					48
757 758 759 760 761	Asp	ATT	CAG	CTG	ACC Thr	CAG	TCT	CCA	TCC	TCC Ser	CTG				Val		48
757 758 759 760 761 762		ATT	CAG	CTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT					48
757 758 759 760 761	Asp 1	ATT Ile	CAG Gln	CTG Leu	ACC Thr 5	CAG Gln	TCT Ser	CCA Pro	TCC Ser	TCC Ser 10	CTG Leu	TCT	Ala	Ser	Val 15	Gly	48 96
757 758 759 760 761 762 763	Asp 1 GAC	ATT Ile AGA	CAG Gln GTC	CTG Leu ACC	ACC Thr 5	CAG Gln ACT	TCT Ser	CCA Pro	TCC Ser	TCC Ser 10	CTG Leu CAG	TCT Ser	Ala ATT	Ser	Val 15 ACT	Gly TAT	
757 758 759 760 761 762 763 764	Asp 1 GAC	ATT Ile AGA	CAG Gln GTC	CTG Leu ACC	ACC Thr 5	CAG Gln ACT	TCT Ser	CCA Pro	TCC Ser	TCC Ser 10	CTG Leu CAG	TCT Ser	Ala ATT	Ser	Val 15 ACT	Gly TAT	
757 758 759 760 761 762 763 764 765	Asp 1 GAC	ATT Ile AGA	CAG Gln GTC	CTG Leu ACC Thr	ACC Thr 5	CAG Gln ACT	TCT Ser	CCA Pro	TCC Ser GCA Ala	TCC Ser 10	CTG Leu CAG	TCT Ser	Ala ATT	Ser AGC Ser	Val 15 ACT	Gly TAT	
757 758 759 760 761 762 763 764 765 766 767	Asp 1 GAC Asp	ATT Ile AGA Arg	CAG Gln GTC Val	CTG Leu ACC Thr 20	ACC Thr 5 ATC Ile	CAG Gln ACT Thr	TCT Ser TGC Cys	CCA Pro CGG Arg	TCC Ser GCA Ala 25 GGG	TCC Ser 10 AGT Ser	CTG Leu CAG Gln	TCT Ser GGC Gly	Ala ATT Ile	AGC Ser 30	Val 15 ACT Thr	Gly TAT Tyr	
757 758 759 760 761 762 763 764 765 766 767 768 769	Asp 1 GAC Asp	ATT Ile AGA Arg	CAG Gln GTC Val	CTG Leu ACC Thr 20	ACC Thr 5 ATC Ile	CAG Gln ACT Thr	TCT Ser TGC Cys	CCA Pro CGG Arg CCA Pro	TCC Ser GCA Ala 25 GGG	TCC Ser 10 AGT Ser	CTG Leu CAG Gln	TCT Ser GGC Gly	ATT Ile AAG Lys	AGC Ser 30	Val 15 ACT Thr	Gly TAT Tyr	96
757 758 759 760 761 762 763 764 765 766 767 768 769 770	Asp 1 GAC Asp	ATT Ile AGA Arg	CAG Gln GTC Val	CTG Leu ACC Thr 20	ACC Thr 5 ATC Ile	CAG Gln ACT Thr	TCT Ser TGC Cys	CCA Pro CGG Arg	TCC Ser GCA Ala 25 GGG	TCC Ser 10 AGT Ser	CTG Leu CAG Gln	TCT Ser GGC Gly	Ala ATT Ile	AGC Ser 30	Val 15 ACT Thr	Gly TAT Tyr	96
757 758 759 760 761 762 763 764 765 766 767 768 769 770 771	Asp GAC Asp TTA Leu	ATT Ile AGA Arg AGT Ser	CAG Gln GTC Val TGG Trp 35	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAG Gln	CAG Gln ACT Thr CAG Gln	TCT Ser TGC Cys AAA Lys	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly	TCC Ser 10 AGT Ser AAA Lys	CTG Leu CAG Gln GCC Ala	TCT Ser GGC Gly CCT Pro	ATT Ile AAG Lys 45	AGC Ser 30 CTC Leu	Val 15 ACT Thr CTG Leu	Gly TAT Tyr ATC	96 144
757 758 759 760 761 762 763 764 765 766 767 768 769 770 771	Asp GAC Asp TTA Leu	ATT Ile AGA Arg AGT Ser	CAG Gln GTC Val TGG Trp 35	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAG Gln	CAG Gln ACT Thr CAG Gln	TCT Ser TGC Cys AAA Lys	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly	TCC Ser 10 AGT Ser AAA Lys	CTG Leu CAG Gln GCC Ala	TCT Ser GGC Gly CCT Pro	Ala ATT Ile AAG Lys 45	AGC Ser 30 CTC Leu	Val 15 ACT Thr CTG Leu	Gly TAT Tyr ATC Ile	96
757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773	Asp GAC Asp TTA Leu	ATT Ile AGA Arg AGT Ser TAT Tyr	CAG Gln GTC Val TGG Trp 35	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAG Gln	CAG Gln ACT Thr CAG Gln	TCT Ser TGC Cys AAA Lys GCA Ala	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly	TCC Ser 10 AGT Ser AAA Lys	CTG Leu CAG Gln GCC Ala	TCT Ser GGC Gly CCT Pro	Ala ATT Ile AAG Lys 45	AGC Ser 30 CTC Leu	Val 15 ACT Thr CTG Leu	Gly TAT Tyr ATC Ile	96 144
757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774	Asp GAC Asp TTA Leu	ATT Ile AGA Arg AGT Ser	CAG Gln GTC Val TGG Trp 35	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAG Gln	CAG Gln ACT Thr CAG Gln	TCT Ser TGC Cys AAA Lys	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly	TCC Ser 10 AGT Ser AAA Lys	CTG Leu CAG Gln GCC Ala	TCT Ser GGC Gly CCT Pro	Ala ATT Ile AAG Lys 45	AGC Ser 30 CTC Leu	Val 15 ACT Thr CTG Leu	Gly TAT Tyr ATC Ile	96 144
757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775	Asp 1 GAC Asp TTA Leu TAT Tyr	ATT Ile AGA Arg AGT Ser TAT Tyr	CAG Gln GTC Val TGG Trp 35 GCA Ala	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAG Gln AGT Ser	CAG Gln ACT Thr CAG Gln TTG Leu	TCT Ser TGC Cys AAA Lys GCA Ala 55	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly GGG Gly	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG Gln GCC Ala CCA Pro	TCT Ser GGC Gly CCT Pro	Ala ATT Ile AAG Lys 45 AGG Arg	AGC Ser 30 CTC Leu TTC Phe	Val 15 ACT Thr CTG Leu AGC Ser	TAT Tyr ATC Ile GGC Gly	96 144
757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774	Asp GAC Asp TTA Leu TAT Tyr	AGA Arg AGT Ser TAT Tyr 50	CAG Gln GTC Val TGG Trp 35 GCA Ala	CTG Leu ACC Thr 20 TAT Tyr AAC Asn	ACC Thr 5 ATC Ile CAG Gln AGT Ser	CAG Gln ACT Thr CAG Gln TTG Leu	TCT Ser TGC Cys AAA Lys GCA Ala 55	CCA Pro CGG Arg CCA Pro 40 AGT Ser	TCC Ser GCA Ala 25 GGG Gly GGG Gly	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG Gln GCC Ala CCA Pro	TCT Ser GGC Gly CCT Pro	Ala ATT Ile AAG Lys 45 AGG Arg	AGC Ser 30 CTC Leu TTC Phe	Val 15 ACT Thr CTG Leu AGC Ser	TAT Tyr ATC Ile GGC Gly	96 144 192
757 758 759 760 761 762 763 764 765 766 767 768 770 771 772 773 774 775	Asp GAC Asp TTA Leu TAT Tyr	AGA Arg AGT Ser TAT Tyr 50	CAG Gln GTC Val TGG Trp 35 GCA Ala	CTG Leu ACC Thr 20 TAT Tyr AAC Asn	ACC Thr 5 ATC Ile CAG Gln AGT Ser	CAG Gln ACT Thr CAG Gln TTG Leu	TCT Ser TGC Cys AAA Lys GCA Ala 55	CCA Pro CGG Arg CCA Pro 40 AGT Ser	TCC Ser GCA Ala 25 GGG Gly GGG Gly	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG Gln GCC Ala CCA Pro	TCT Ser GGC Gly CCT Pro TCA Ser 60	Ala ATT Ile AAG Lys 45 AGG Arg	AGC Ser 30 CTC Leu TTC Phe	Val 15 ACT Thr CTG Leu AGC Ser	TAT Tyr ATC Ile GGC Gly	96 144 192
757 758 759 760 761 762 763 764 765 766 777 778 779 771 772 773 774 775 776	Asp GAC Asp TTA Leu TAT Tyr AGT Ser	AGA Arg AGT Ser TAT Tyr 50	CAG Gln GTC Val TGG Trp 35 GCA Ala	CTG Leu ACC Thr 20 TAT Tyr AAC Asn	ACC Thr 5 ATC Ile CAG Gln AGT Ser	CAG Gln ACT Thr CAG Gln TTG Leu	TCT Ser TGC Cys AAA Lys GCA Ala 55	CCA Pro CGG Arg CCA Pro 40 AGT Ser	TCC Ser GCA Ala 25 GGG Gly GGG Gly	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG Gln GCC Ala CCA Pro	TCT Ser GGC Gly CCT Pro TCA Ser 60	Ala ATT Ile AAG Lys 45 AGG Arg	AGC Ser 30 CTC Leu TTC Phe	Val 15 ACT Thr CTG Leu AGC Ser	TAT Tyr ATC Ile GGC Gly	96 144 192 240
757 758 759 760 761 762 763 764 765 766 767 768 770 771 772 773 774 775 776 777	Asp GAC Asp TTA Leu TAT Tyr AGT Ser 65	ATT Ile AGA Arg AGT Ser TAT Tyr 50 GGA Gly	CAG Gln GTC Val TGG Trp 35 GCA Ala	CTG Leu ACC Thr 20 TAT Tyr AAC Asn	ACC Thr 5 ATC Ile CAG Gln AGT Ser	CAG Gln ACT Thr CAG Gln TTG Leu GAA Glu 70	TCT Ser TGC Cys AAA Lys GCA Ala 55 TTC Phe	CCA Pro CGG Arg CCA Pro 40 AGT Ser	TCC Ser GCA Ala 25 GGG Gly GGG Gly CTC Leu	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG Gln GCC Ala CCA Pro	TCT Ser GGC Gly CCT Pro TCA Ser 60	Ala ATT Ile AAG Lys 45 AGG Arg	AGC Ser 30 CTC Leu TTC Phe	Val 15 ACT Thr CTG Leu AGC Ser	TAT Tyr ATC Ile GGC Gly CCT Pro 80	96 144 192

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781 782 783	Glu	Asp	Ser	Ala	Thr 85	Tyr	Tyr	Сув	Gly	Gln 90	Gly	Asn	Ser	Tyr	Pro 95	Leu	
784				GGA													324
785 786	Thr	Phe	Gly	Gly 100	Gly	Thr	Lys	Val	Glu 105	Ile	Lys	Arg					
787									105								
788	′ 0	\ - >-															
789 790	(2) IN	FORM	ATIO	N FO	R SE	Õ ID	NO:	18:								
791			(i)	SEQUI	ENCE	CHA	RACT	ERIS'	rics	:							
792 793					-		: 100 amin		-	acid	8						
794				(B)			GY:										
795																	
796 797		(:	ii)	MOLE	CULE	TYP	E: p	rote:	in								
798		(:	xi)	SEQUI	ENCE	DES	CRIP:	rion	: SE	Q ID	NO:	18:					
799				_			_	_	_	_	_	_		_			
800 801	Asp 1	Ile	GIn	Leu	Thr 5	GIn	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15	GIY	
802	-				J												
803 804	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg		Ser	Gln	Gly	Ile		Thr	Tyr	
805				20					25					30			
806	Leu	Ser	_	Tyr	Gln	Gln	Lys		Gly	Lys	Ala	Pro	_	Leu	Leu	Ile	
807 808			35					40					45				
809	Tyr	Tyr	Ala	Asn	Ser	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
810		50					55					60					
811 812	Ser	Glv	Ser	Gly	Thr	Glu	Phe	Thr	T.e.u	Thr	Tle	Ser	Ser	T.e.	Gln	Pro	
813	65	1	202	1		70					75					80	
814	a 1	3	0	31-	mb	M		~	a1	a 1	a1	3	g		Desc	T	
815 816	GIU	Asp	ser	Ala	85	TYF	TYF	Cys	GIY	90	GIY	ASD	ser	TYL	95	Leu	
817																	
818 819	Thr	Phe	Gly	Gly 100	Gly	Thr	Lys	Val	Glu 105	Ile	Lys	Arg					
820				100					103								
821	(2)) IN	FORM	ATIO	V FOI	R SE	Q ID	NO:	19:								
822 823		(;) SE	OUEN	כוב כו	HARA	מייצר:	rstt(cs:								
824		`-	(.	A) LI	ENGTI	H: 3	24 ba	ase]	pair	3							
825				B) T													
826 827			•	C) 57 D) T(1								
828																	
829 830		(ii) MO	LECUI	LE T	YPE:	CDN	A									
831		(iii) HY:	РОТНІ	ETIC	AL: 1	NO										
832																	

Raw Sequence Listing

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833 834		(iv) AN	TI-S	ENSE	: NO											
835																	
836		/ 4 1	\ mm	3 M1110 1	a .												
837		(IX		ATURI		72 TO 32 .	ana										
838				A) N	•			224									
839			()	B) L	JCAI.	TON:	⊥	344									
840																	
841		/d 1	\ CE/	OTTERT	7 TO 101	maan.	T DM T	337 - 1		TD 17	0.10						
842		(XI,) SE	QUEN	JE D	ESCR.	TLTT	JN: i	SEQ.	TD M	2:19	:					
843	as a) mm	a a	ama.	3.00	as a	mam	<i>a</i> a,	maa	mam	a. a	mam	a a.	mam	am.	a a.	4.0
844				CTG													48
845	Asp 1	TIE	GIII	Leu		GIII	Ser	Pro	ser			ser	ATA	ser		GIA	
846					5					10	•				15		
847	C A C	202	CITIC!	3.00	א חיים	3 CITI	maa.	a a	000	3 CITI	<i>(</i> 13.3	3.00	amm	3.00	337	m > m	0.0
848				ACC													96
849	ABD	Arg	vai	Thr 20	TIE	Inr	Cys	GIII		ser	GIII	ser	Leu		ABII	Tyr	
850				20					25					30			
851	תייים	አአጥ	TICC	TAT	C A C	CAC	***	CCA	aaa	***	a mm	COM	330	ama	ama	3 000	144
852																	144
853	теа	ASII	35	Tyr	GIII	GIII	гув	40	GTA	гув	тте	Pro	_	Leu	Leu	TIE	
854			33					40					45				
855	mam	3.00	CCA	TCC	3 CIT	mm/d	CA A	» cm	aaa	2 111111	000	mam	000	mma	3.00	000	100
856																	192
857	TÄT	50	ALA	Ser	Ser	теп	55	ser	GIY	тте	PIO		Arg	Pne	ser	GIY	
858		50					55					60					
859	3 CIT	CC3	m/m	aaa	3.00	CATT	mma	3.00	ama	3.00	3.00	3.00	3.00	ama	a. a	aam	240
860				GGG													240
861	65	GIY	Ser	Gly	Inr		Pne	THE	Leu	THE		ser	ser	ьęц	GIN		
862	03					70					75					80	
863	GAA	CAT	ффф	GCC	א כיייי	יייגייי	ሞአሮ	тСт	CAG	CAT	አአጥ	ጥአጥ	COT	אככ	CCT	CTC	288
864			2	Ala													200
865	GIU	reb	1116	AIG	85	TYT	TYL	Cys	GIII	90	ADII	TYL	GIY	1111	95	пеп	
866					0,5					30					93		
867	ΣСТ	ጥጥር	aac	GGA	aaa	A CC	AAG	стс	GAG	ልጥሮ	222	CGA					324
868				Gly													344
869	1111	1116	GLY	100	GLY	* ***	шув	Val	105	116	цур	Arg					
870				100					103								
871																	
872	(2)	TNI	TORM:	ATIO	ያ ፑርነ	R SEC	חד ר	NO ·	20 •								
873	(2)		. 0141	11101		,	2 22	110.									
874			(i) 9	SEOUI	ENCE	CHAI	RACTI	ZRTS'	rtcs.	•							
875			·-/ •	-		NGTH					3						
876						PE: a					•						
877						POLO											
878				(-,													
879		(+	ii) 7	MOLE	TULE	ТУРІ	ימ : פ	cote	in								
880		, -	, -				__					•					
881		(3	ci) s	SEQUE	ENCE	DESC	RIP	CION	SEC) ID	NO:2	20:					
882		,-	, -			,			,		• • •	•					
883	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Gln	Ser	Ala	Ser	Val	Glv	
884	1				5					10					15	2	
	_				_												

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885																		
886	Asp	Arg	Val		Ile	Thr	Cys	Gln		Ser	Gln	Ser	Leu		Asn	Tyr		
887				20					25					30				
888	_	_	_				_	_		_			_	_	_			
889	Leu	Asn	_	Tyr	Gln	Gln	Lys		Gly	Lys	Ile	Pro	_	Leu	Leu	Ile		
890			35					40					45					
891	_	_		_	_	_		_			_	_	_		_			
892	Tyr	Arg	Ala	Ser	Ser	Leu		Ser	Gly	Ile	Pro		Arg	Phe	Ser	Gly		
893		50					55					60						
894	_		_						_			_	_	_		_		
895		Gly	Ser	Gly	Thr		Phe	Thr	Leu	Thr		Ser	Ser	Leu	GIn			
896	65					70					75					80		
897	~3		-,		-1		_	—	~ 1				41					
898	GIU	Asp	Pne	АТа		Tyr	ıyr	Сув	GIN		Asn	Tyr	GIĀ	Thr		Leu		
899					85					90					95			
900	m\2	5 % -	~ 1	~ 1	~1	m\	T	*** 7	~1	T1.	T	3						
901 902	Int	Phe	GIY	100	GIY	Inr	пЛя	VAIT	105	TTA	гув	Arg						
				100					103									
903 904	(2)) INI	PODM	N TT ()	T E/O	0.00	. TD	NO.										
905	(2)	, THI	·OKIM	RIIOI	N FOI	K DE	עד ג	NO:	6 T .									
906		/43	\ C12/	QUEN	ים כו	אמסגע	יסקייי.	remt <i>i</i>	7Q.									
907		(- /	•	A) Li						8								
908				B) T				-		-								
909			-	c) s:														
910			•	D) TO					•									
911			``	, -	J_													
912		(ii)	MOI	LECUI	LE T	YPE:	DNA	(ge	nomi	c)								
913		,,						, 5		-,								
914																		
915		(ix)) FE	ATURI	3:													
916			(2	A) N	AME/I	KEY:	CDS											
917				B) L				324										
918																		
919		(xi)	SE	QUEN	CE DI	ESCR:	IPTI	ON:	SEQ :	ID N	0:21	:						
920				-					_									
921	GAC	ATTC	AGC :	rgac(CCAG	rc To	CCAC'	CTC	CT	GCCC	GTCA	GTC:	rtgg:	AGA (GTCG	GCCTC	C	60
922																		
923	ATC:	ICCT 1	I MM	INNNN	INNNN	IN NN	INNN	INNN	NN N	INNN	NNNN	NNN	INNN	NNN I	INNNN	NNNNN	N	120
924																		
925	NNN	INNNN	NNN I	INNNN	INNN	NN NI	INNNN	MNNN	NN R	INNNN	NNNN	NNN	INNN	NNN I	NNTC	CCAGA	C	180
926																		
927	AGG'	TTCA	CTG (GCAG'	rggg'	TC A	GGCA(CTGA:	r TT	CACA	CTGA	AAA'	rcag(CAG	AGTG	GAGGC	T	240
928																		
929	GAG	GATG:	rtg (GGGT'	rtat'	TA C	rgca:	rgca:	A GC	rctt(CGGT	CTC	CTTG	GAC (GTTC	GGCCA	A	300
930																		
931	GGG	ACCAI	AGG :	rgga.	AATC	AG A	CGA											324
932																		
933																		
934	(2)) IN	FORM	ATIO	N FO	R SE	D ID	NO:	22:									
935																		
47 F		(i '	1 CT/	OTTEN	יום אי	и в в в в	יידע אירי	TSTT(~Q •									



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Raw Sequence Listing

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937 938		(A)) LEI		: 100 amino			acid	8							
939		(D)	TOI	POLO	GY: :	line	ar									
940																
941	(ii)	MOL	ECULI	E TY	PE: j	prot	ein									
942																
943	(xi)	SEQ	JENCI	E DE	SCRI	PTIO	N: S	EQ II	ON C	:22:						
944																
945	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly
946	1				5					10					15	
947																
948	Glu	Ser	Ala	Ser	Ile	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
949				20					25					30		
950																
951	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa		Xaa	Xaa	Xaa	Xaa		Xaa	Xaa	Xaa
952			35					40					45			
953											_	_				
954	Xaa		Xaa	Xaa	Xaa	Xaa		Xaa	Xaa	Xaa	Pro		Xaa	Xaa	Thr	Xaa
955		50					55					60				
956		••••			••		77	 .	**			17	•	••- 7	~1	
957		Xaa	Xaa	Xaa	Xaa		Xaa	Xaa	xaa	ràs		xaa	Arg	vaı	GIU	
958 050	65					70					75					80
959 960	Vaa	Vaa	Val	~1··	37-1	Vaa	Vaa	Vaa	Wat	Vaa	71-	T 011	7 ~~	g.~	Dro	Two
961	Add	Aaa	vai	GIY	85	naa	Aaa	naa	Mec	90	ALG	пеп	Arg	per	95	пр
962					0.5					30					93	
963	Yaa	Yaa	Xaa	Yaa	Yaa	Yaa	T.vg	Val	Yaa	Yaa	Arα	Ara				
964	nuu		1144	100	11.44	1144	_,	,	105	1144	9	9				
965																
966																
967	(2) INF	ORMA'	TION	FOR	SEQ	ID 1	NO:2	3:								
968					_											
969	(i)	SEQ	JENCI	E CH	ARAC:	TERI:	STIC	S:								
970		(A)) LEI	NGTH	: 324	4 ba	ве ра	airs								
971		(B)	TYI	PE: 1	nucle	eic a	acid									
972		(C)	STI	RANDI	EDNE	5S: 1	both									
973		(D)	TOI	POLO	GY: :	line	ar									
974																
975	(ii)	MOL	ECULI	E TY	PE: 0	CDNA										
976																
977	(iii)	HYP	OTHE:	rica:	L: NO)										
978																
979	(iv)	ANT:	I-SEI	NSE:	МО											
980																
981																
982	(ix)					an.c										
983) NAI	•			2.4									
984		(B) LO	JATI(JN:	13	4									
985 086																
986 987	/2 \	ano.	יייינשוי	ימת מ	-	יסדית	λΤ. C'	₽ ∧ T '	- NT	. 22 -						
987 988	(xi)	SEQ.	OENCI	e nr:	PCKT	FITO	N: 5	e'⊼ Tì	O MO	: 43:						
300																

Raw Sequence Listing

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989 990 991 992			CAG Gln														48
993 994 995 996			GTC Val														96
997 998 999 1000			TGG Trp 35													-	144
1001 1002 1003 1004			GCA Ala														192
1005 1006 1007 1008			TCT Ser														240
1009 1010 1011 1012			TTT Phe														288
1013 1014 1015 1016			GGC Gly														324
1017 1018 1019	(2)	IN	FORM	TION	1 FOF	R SEÇ) ID	NO:2	24:								
1020 1021 1022 1023		1	(i) £	(A) (B)		NGTH:	: 108 amino	ami aci	ino a id	: acids	3						
1024 1025 1026 1027			li) B				_			O ID	NO:2	24:					
1028 1029 1030 1031	Asp 1		Gln	-									Ala	Ser	Val 15	Gly	
1032 1033 1034	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Arg	Ala 25	Ser	Gln	Gly	Ile	Ser 30	Asp	Tyr	
1035 1036 1037			Trp 35	_			_	40	_	_			45				
1038 1039 1040	Tyr	Ala 50	Ala	Ser	Ser	Leu	Gln 55	Ser	Gly	Val	Pro	Ser 60	Arg	Phe	Ser	Gly	

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1041	Ser Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
1042	65				70					75					80	
1043																
1044	Glu Asp	Phe	Ala	Thr	Tyr	Tyr	Сув	Leu	Gln	Gly	Tyr	Gly	Thr	Pro	Tyr	
1045				85					90					95		
1046																
1047	Ser Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
1048			100					105								
1049																
1050	(2) IN	FORM	ATIO	N FOI	R SE	Q ID	NO:	25:								
1051																
1052	(i) SE	-													
1053			A) LI				-	•	3							
1054		-	B) T													
1055		-	C) S:					n.								
1056		(1	D) T	OPOL	OGY:	line	ear									
1057																
1058	(ii) MO	LECUI	LE T	YPE:	cDN	A									
1059																
1060	(iii) HY	POTH	ETIC	AL: 1	10										
1061																
1062	(iv) AN	ri-si	ENSE	: NO											
1063																
1064																
1065	(ix) FE														
1066			A) N													
1067		(1	B) L(OCAT:	CON:	13	324									
1068																
1069		_														
1070	(xi) SE	QUEN	CE DI	ESCR:	[PTIC	ON: S	SEQ :	ID NO	0:25	:					
1071																
1072	GAC ATT															48
1073	Asp Ile	Gln	Leu		Gln	Ser	Pro	Ser		Leu	Ser	Ala	Ser		Gly	
1074	1			5					10					15		
1075																
1076	GAC ACA															96
1077	Asp Thr	Val		Ile	Thr	Сув	Arg		Ser	Gln	Asp	Ile		Asn	Asn	
1078			20					25					30			
1079																
1080	TTA GTC															144
1081	Leu Val	_	Tyr	Gln	Gln	Lys		Gly	Lys	Ala	Pro	_	Leu	Leu	Ile	
1082		35					40					45				
1083															~~~	100
1084	TAT GCT															192
1085	Tyr Ala		Ser	Arg	Leu		Asp	GŢĀ	Val	Pro		Arg	Pne	ser	GIY	
1086	50					55					60					
1087														 -		
1088	AGT GGG															240
1089	Ser Gly	Ser	Gly	Thr		Phe	Thr	Leu	Thr		Asn	Pro	Val	Glu		
1090	65				70					75					80	
1091				 –					 - ~	_ ~-					a ~~	
1092	GAC GAT	GCT	GCG	GAT	TAC	TAC	TGT	CTA	CAG	ACT	AAG	AGT	TCT	CCT	CGG	288

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1093 1094 1095	Asp Asp	Ala	Ala	Asp 85	Tyr	Tyr	Сув	Leu	Gln 90	Thr	Lys	Ser	Ser	Pro 95	Arg	
1096	ACG TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	CGA					324
1097	Thr Phe															.
1098			100	1		-,, -		105		-,-	5					
1099															*	
1100																
1101	(2) IN	FORM	ATTO	N FOI	R SEC	מד כ	NO:	26:								
1102	(-,					E		- • •								
1103		(i)	SEQUI	ENCE	CHAI	RACTI	ERIS'	TICS	:							
1104		(-,) LEI						3						
1105				TY!						_						
1106) TO												
1107			•													
1108	(ii) 1	MOLE	CULE	TYP	E: p:	rote:	in								
1109	•	-				•										
1110	(xi)	SEOUI	ENCE	DES	CRIP'	TION	: SE	Q ID	NO:2	26:					
1111	,	,							•							
1112	Asp Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1113	ī			5					10					15	-	
1114																
1115	Asp Thr	Val	Thr	Ile	Thr	Сув	Arq	Ala	Ser	Gln	Asp	Ile	Ser	Asn	Asn	
1116	-		20			•	•	25			•		30			
1117																
1118	Leu Val	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
1119		35	_			_	40	_	_			45				
1120																
1121	Tyr Ala	Ala	Ser	Arg	Leu	Gln	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
1122	50			_		55	_	_			60	_			_	
1123																
1124	Ser Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Pro	Val	Glu	Ala	
1125	65				70					75					80	
1126																
1127	Asp Asp	Ala	Ala	Asp	Tyr	Tyr	Сув	Leu	Gln	Thr	Lys	Ser	Ser	Pro	Arg	
1128				85					90					95		
1129																
1130	Thr Phe	Gly	${\tt Gln}$	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
1131			100					105								
1132																
1133	(2) IN	FORM	ATIO	N FOI	R SE	QID	NO:	27:								
1134																
1135	(i) SE	-													
1136			A) LI						8							
1137		-	B) T													
1138		•	C) S					h.								
1139		(1	D) T	OPOL	OGY:	line	ear									
1140		_						_	_							
1141	(ii) MO:	LECUI	LE T	YPE:	DNA	(ge	nomi	c)							
1142																
1143				_												
1144	(ix) FE	ATURI	E :												

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1145		(A) NAM	ME/KE	EY: (CDS											
1146		(B) LO	CATIO	ON: I	132	24										
1147																
1148	(ix) F	EATURE:	:													
1149		(A) NAI	ME/KE	ZY: r	nat j	pept:	ide									
1150		(B) LO	CATIO	ON: 3	31	324										
1151																
1152																
1153	(xi) S	EOUENCI	E DES	CRI	PTIO	N: SI	EO II	O NO	:27:							
1154	,,															
1155	GACATTCAGC	TGACC	CAGTO	TC	ANN	NNNN	NNN	NNNN	NNN I	INNNN	NNN	NN NI	MMMM	NNNN	1	60
1156																
1157	NNNNNNNNN	NNNNN	MNNN	I NN	MMM	NNNN	NNN	NNNN	NNN I	NNNN	NNNN	NN NI	NNNN	MMM	4	120
1158			*******				-101212								•	
1159	NNNNNNNNN	NNCAGO	יכפייי	r GAT	ימייי	TGAG	GTT	TCCA:	ACC (GGGC(тст	GG AG	TCCC	CAGAC	7	180
1160		111.0110.													-	
1161	AGGTTCAGTG	GCAGTO	CGTC	r ggz	CAC	ГСАТ	ттс	ACAC'	TCA Z	AAATO	TAGC	AG A	зтаса	AGGC	r	240
1162	AUGIICAGIO	CONCI				- 0.1.1	1101						J 1 0 02		•	
1163	GAGGATGTTG	מממיייי	ר א ייי די צי	У СТО	ግር ል ጥ <i>ር</i>	2022	тът	ארארי	י מיטמ	דידיכי	יייייי א	יידי יים	יייר <i>יכ</i> נ	2000	~	300
1164	GAGGAIGIIG	GGGII.	LALL		JOHL	JUM	+444		nun .	1100	11101		1100		_	300
1165	GGGACCAAAC	тссат	ልጥሮል ፣	א אכינ	22											324
1166	GGGACCHIAC	IGGAIL	···	· nc	JA											721
1167	(2) INFOR	MATTON	₽∩¤	SEO.	ו חד	VO • 21	ρ.									
1168	(Z) INFOR	MITON	FOR	250	10 1	.10.2	٠.									
1169	(i) a	EQUENCI	י מטי	אם א פין	ידסקי	CTT (C	e.									
1170	• •	(A) LEI						~								
1171		(B) TYI					actu	9								
1172		(D) TO														
1172		(D) 101	OLOC	31		21										
1174	/44\ W	OLECULI	e mvi	D	~~~+	ai n										
1175	(II) M	OUPCODI	2 111		TOU	STII										
1176																
1177	•															
1177	/i\ c	EQUENCI	2 DEC	T CO	ו∧דתו	NT. C1	PA T1	D 310	. 20.							
1178	(XI) S	POOPNC	s Des	CKI	71101	M: 91	eā II	D NO	: 40:							
11/9	3 am T	1. 01.	T 011	mb	~1 =	C 0 m	Dwa	Vaa	Vaa	V	Vaa	Vaa	Vaa	Vaa	Vaa	
1181	Asp I	le Gln	пеп	5	GIII	Ser	PIO	naa	10	naa	Aaa	Aaa	naa	15	Aaa	
1182	1			5					10					TO		
	V V	V	V	V	V	Vaa	V	v	Vaa	Vaa	Vaa	Vaa	Vaa	Vaa	Vaa	
1183	лаа л	aa Xaa		Add	лаа	Add	Add		Add	Add	Add	Add		naa	Add	
1184			20					25					30			
1185	W W	٧	77	v	W	V	V	¥	V	V	V	71 -	Dma	T 0	T10	
1186	хаа х	aa Xaa	xaa	хаа	лаа	лаа		Aaa	лаа	Add	Add		Pro	теп	TTG	
1187		35					40					45				
1188		1	a	.	3		a	ai	77-7	D	3	3	nh-	a	03	
1189		lu Val	ser	Asn	Arg		ser	GTĀ	val	PTO		Arg	Fue	ser	GTÅ	
1190	5	U				55					60					
1191			_		_			_	_		_			~ ?	. 7 -	
1192		ly Ser	Asp	Thr		Phe	Thr	Leu	ГĀВ		ser	Arg	vaı	Glu		
1193	65				70					75					80	
1194	-				_	_	_			_		•		_	_1	
1195	Glu A	sp Val	GTA		Tyr	Tyr	Cys	Met		ıyr	Thr	H18	тте		rne	
1196				85					90					95		

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1198 1199 1200																
	I	hr Ph	e Gl	y Pro	o Gl	y Th	r Ly	s Le	ı Ası	o Ile	e Lya	s Arg	3			
1200				10	0				10	5						
1201																
1202																
1203																
1204	(2) I	NFORM	ATIO	N FO	R SE	Q ID	NO:	29:								
1205																
1206	(i) SE	-													
1207			A) L				_	_	3							
1208		•	B) T													
1209		•	C) S					h								
1210		(D) T	OPOL	OGY:	line	ear									
1211																
1212	(i	i) MO	LECU	LE T	YPE:	cDN	A									
1213																
1214	(ii	i) HY	POTH	ETIC	AL: 1	10										
1215																
1216	(i	v) AN	TI-S	ENSE	: NO											
1217																
1218																
1219	(i	x) FE														
1220		•	A) N	•												
1221		(B) L	OCAT:	ON:	1	324									
1222																
1223																
1224	(ж	i) SR	\sim ttent/	75 70												
		-, U	QOEM,	CE DI	≤SCR.	LPTIC	ON: S	SEQ 1	ED NO	0:29	•					
1225			_					_								
1226	GAC AT	T CAG	CTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT					48
1226 1227	Asp Il	T CAG	CTG	ACC Thr	CAG	TCT	CCA	TCC	TCC Ser	CTG	TCT			Val		48
1226 1227 1228		T CAG	CTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT					48
1226 1227 1228 1229	Asp Il	T CAG e Gln	CTG Leu	ACC Thr 5	CAG Gln	TCT Ser	CCA Pro	TCC Ser	TCC Ser 10	CTG Leu	TCT Ser	Ala	Ser	Val 15	Gly	
1226 1227 1228 1229 1230	Asp II 1 GAC AG	T CAG e Gln A GTC	CTG Leu ACC	ACC Thr 5	CAG Gln ACT	TCT Ser	CCA Pro	TCC Ser	TCC Ser 10	CTG Leu CAG	TCT Ser	Ala ATT	Ser	Val 15	Gly TAT	4 8 96
1226 1227 1228 1229 1230 1231	Asp Il	T CAG e Gln A GTC	CTG Leu ACC Thr	ACC Thr 5	CAG Gln ACT	TCT Ser	CCA Pro	TCC Ser GCA Ala	TCC Ser 10	CTG Leu CAG	TCT Ser	Ala ATT	Ser AGC Ser	Val 15	Gly TAT	
1226 1227 1228 1229 1230 1231 1232	Asp II 1 GAC AG	T CAG e Gln A GTC	CTG Leu ACC	ACC Thr 5	CAG Gln ACT	TCT Ser	CCA Pro	TCC Ser	TCC Ser 10	CTG Leu CAG	TCT Ser	Ala ATT	Ser	Val 15	Gly TAT	
1226 1227 1228 1229 1230 1231 1232 1233	Asp II 1 GAC AG Asp Ar	T CAG e Gln A GTC g Val	CTG Leu ACC Thr 20	ACC Thr 5 ATC	CAG Gln ACT Thr	TCT Ser TGC Cys	CCA Pro CGG Arg	TCC Ser GCA Ala 25	TCC Ser 10 AGT Ser	CTG Leu CAG Gln	TCT Ser AGC Ser	Ala ATT Ile	AGC Ser 30	Val 15 AAT Asn	Gly TAT Tyr	96
1226 1227 1228 1229 1230 1231 1232 1233 1234	Asp II GAC AG Asp Ar	T CAG e Gln A GTC g Val	CTG Leu ACC Thr 20	ACC Thr 5 ATC Ile	CAG Gln ACT Thr	TCT Ser TGC Cys	CCA Pro CGG Arg	TCC Ser GCA Ala 25	TCC Ser 10 AGT Ser	CTG Leu CAG Gln	TCT Ser AGC Ser	Ala ATT Ile	AGC Ser 30	Val 15 AAT Asn	Gly TAT Tyr	
1226 1227 1228 1229 1230 1231 1232 1233 1234 1235	Asp II 1 GAC AG Asp Ar	T CAG e Gln A GTC g Val T TGG n Trp	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile	CAG Gln ACT Thr	TCT Ser TGC Cys	CCA Pro CGG Arg CCA Pro	TCC Ser GCA Ala 25	TCC Ser 10 AGT Ser	CTG Leu CAG Gln	TCT Ser AGC Ser	Ala ATT Ile CAG Gln	AGC Ser 30	Val 15 AAT Asn	Gly TAT Tyr	96
1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236	Asp II GAC AG Asp Ar	T CAG e Gln A GTC g Val	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile	CAG Gln ACT Thr	TCT Ser TGC Cys	CCA Pro CGG Arg	TCC Ser GCA Ala 25	TCC Ser 10 AGT Ser	CTG Leu CAG Gln	TCT Ser AGC Ser	Ala ATT Ile	AGC Ser 30	Val 15 AAT Asn	Gly TAT Tyr	96
1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237	Asp II GAC AG Asp Ar TTA AA Leu As	T CAG e Gln A GTC g Val T TGG n Trp 35	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAA Gln	CAG Gln ACT Thr CAG Gln	TCT Ser TGC Cys AAA Lys	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly	TCC Ser 10 AGT Ser AAA Lys	CTG Leu CAG Gln GCC Ala	TCT Ser AGC Ser CCT Pro	Ala ATT Ile CAG Gln 45	AGC Ser 30 CCC Pro	Val 15 AAT Asn TTG Leu	Gly TAT Tyr ATT Ile	96 144
1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238	Asp III GAC AG Asp Ar TTA AA Leu As	T CAG e Gln A GTC g Val T TGG n Trp 35	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAA Gln	CAG Gln ACT Thr CAG Gln	TCT Ser TGC Cys AAA Lys	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly	TCC Ser 10 AGT Ser AAA Lys	CTG Leu CAG Gln GCC Ala	TCT Ser AGC Ser CCT Pro	Ala ATT Ile CAG Gln 45	AGC Ser 30 CCC Pro	Val 15 AAT Asn TTG Leu	Gly TAT Tyr ATT Ile	96
1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239	Asp III GAC AG Asp Ar TTA AA Leu As TAT GA Tyr GI	T CAG e Gln A GTC g Val T TGG n Trp 35 G GTT u Val	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAA Gln	CAG Gln ACT Thr CAG Gln	TCT Ser TGC Cys AAA Lys GCC Ala	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly	TCC Ser 10 AGT Ser AAA Lys	CTG Leu CAG Gln GCC Ala	TCT Ser AGC Ser CCT Pro	Ala ATT Ile CAG Gln 45	AGC Ser 30 CCC Pro	Val 15 AAT Asn TTG Leu	Gly TAT Tyr ATT Ile	96 144
1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240	Asp III GAC AG Asp Ar TTA AA Leu As TAT GA Tyr GI	T CAG e Gln A GTC g Val T TGG n Trp 35	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAA Gln	CAG Gln ACT Thr CAG Gln	TCT Ser TGC Cys AAA Lys	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly	TCC Ser 10 AGT Ser AAA Lys	CTG Leu CAG Gln GCC Ala	TCT Ser AGC Ser CCT Pro	Ala ATT Ile CAG Gln 45	AGC Ser 30 CCC Pro	Val 15 AAT Asn TTG Leu	Gly TAT Tyr ATT Ile	96 144
1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241	Asp II GAC AG Asp Ar TTA AA Leu As TAT GA Tyr GI	T CAG e Gln A GTC g Val T TGG n Trp 35 G GTT u Val	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAA Gln AAC	CAG Gln ACT Thr CAG Gln CGG Arg	TCT Ser TGC Cys AAA Lys GCC Ala 55	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly GGA Gly	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG Gln GCC Ala CCA Pro	TCT Ser AGC Ser CCT Pro GAC Asp 60	Ala ATT Ile CAG Gln 45 AGG Arg	AGC Ser 30 CCC Pro	Val 15 AAT Asn TTG Leu AGT Ser	Gly TAT Tyr ATT Ile GGC Gly	96 144 192
1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242	Asp III GAC AG Asp Ar TTA AA Leu As TAT GA Tyr GI S	T CAG e Gln A GTC g Val T TGG n Trp 35 G GTT u Val 0	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAA Gln AAC Asn	CAG Gln ACT Thr CAG Gln CGG Arg	TCT Ser TGC Cys AAA Lys GCC Ala 55	CCA Pro CGG Arg CCA Pro 40 TCT Ser	TCC Ser GCA Ala 25 GGG Gly GGA Gly	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG Gln GCC Ala CCA Pro	TCT Ser AGC Ser CCT Pro GAC Asp 60	Ala ATT Ile CAG Gln 45 AGG Arg	AGC Ser 30 CCC Pro TTC Phe	Val 15 AAT Asn TTG Leu AGT Ser	Gly TAT Tyr ATT Ile GGC Gly GCT	96 144
1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243	Asp III CAC AG Asp Ar TTA AA Leu As TAT GA Tyr GI AGT GG Ser GI	T CAG e Gln A GTC g Val T TGG n Trp 35 G GTT u Val 0	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAA Gln AAC Asn	CAG Gln ACT Thr CAG Gln CGG Arg	TCT Ser TGC Cys AAA Lys GCC Ala 55	CCA Pro CGG Arg CCA Pro 40 TCT Ser	TCC Ser GCA Ala 25 GGG Gly GGA Gly	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG Gln GCC Ala CCA Pro	TCT Ser AGC Ser CCT Pro GAC Asp 60	Ala ATT Ile CAG Gln 45 AGG Arg	AGC Ser 30 CCC Pro TTC Phe	Val 15 AAT Asn TTG Leu AGT Ser	Gly TAT Tyr ATT Ile GGC Gly GCT Ala	96 144 192
1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244	Asp III GAC AG Asp Ar TTA AA Leu As TAT GA Tyr GI S	T CAG e Gln A GTC g Val T TGG n Trp 35 G GTT u Val 0	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAA Gln AAC Asn	CAG Gln ACT Thr CAG Gln CGG Arg	TCT Ser TGC Cys AAA Lys GCC Ala 55	CCA Pro CGG Arg CCA Pro 40 TCT Ser	TCC Ser GCA Ala 25 GGG Gly GGA Gly	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG Gln GCC Ala CCA Pro	TCT Ser AGC Ser CCT Pro GAC Asp 60	Ala ATT Ile CAG Gln 45 AGG Arg	AGC Ser 30 CCC Pro TTC Phe	Val 15 AAT Asn TTG Leu AGT Ser	Gly TAT Tyr ATT Ile GGC Gly GCT	96 144 192
1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245	Asp III GAC AG Asp Ar TTA AA Leu As TAT GA Tyr GI AGT GG Ser GI	T CAG e Gln A GTC g Val T TGG n Trp 35 G GTT u Val 0 G TCG y Ser	CTG Leu ACC Thr 20 TAT Tyr TCC Ser GAC Asp	ACC Thr 5 ATC Ile CAA Gln AAC Asn	CAG Gln ACT Thr CAG Gln CGG Arg	TCT Ser TGC Cys AAA Lys GCC Ala 55 TTC	CCA Pro CGG Arg CCA Pro 40 TCT Ser	TCC Ser GCA Ala 25 GGG Gly GGA Gly CTC Leu	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG Gln GCC Ala CCA Pro	TCT Ser AGC Ser CCT Pro GAC Asp 60 AGC	Ala ATT Ile CAG Gln 45 AGG Arg	AGC Ser 30 CCC Pro TTC Phe	Val 15 AAT Asn TTG Leu AGT Ser	Gly TAT Tyr ATT Ile GGC Gly GCT Ala 80	96 144 192 240
1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246	Asp III GAC AG Asp Ar TTA AA Leu As TAT GA Tyr GI Ser GI 65	T CAG e Gln A GTC g Val T TGG n Trp 35 G GTT u Val 0 G TCG y Ser	CTG Leu ACC Thr 20 TAT Tyr TCC Ser GAC Asp	ACC Thr 5 ATC Ile CAA Gln AAC Asn ACT Thr	CAG Gln ACT Thr CAG Gln CGG Arg GAT Asp 70	TCT Ser TGC Cys AAA Lys GCC Ala 55 TTC Phe	CCA Pro CGG Arg CCA Pro 40 TCT Ser ACA Thr	TCC Ser GCA Ala 25 GGG Gly CTC Leu	TCC Ser 10 AGT Ser AAA Lys GTC Val AAA Lys	CTG Leu CAG Gln GCC Ala CCA Pro ATC Ile 75	TCT Ser AGC Ser CCT Pro GAC Asp 60 AGC Ser	Ala ATT Ile CAG Gln 45 AGG Arg AGA Arg	AGC Ser 30 CCC Pro TTC Phe GTG Val	Val 15 AAT Asn TTG Leu AGT Ser GAG Glu	Gly TAT Tyr ATT Ile GGC Gly GCT Ala 80 TTC	96 144 192
1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245	Asp III GAC AG Asp Ar TTA AA Leu As TAT GA Tyr GI AGT GG Ser GI	T CAG e Gln A GTC g Val T TGG n Trp 35 G GTT u Val 0 G TCG y Ser	CTG Leu ACC Thr 20 TAT Tyr TCC Ser GAC Asp	ACC Thr 5 ATC Ile CAA Gln AAC Asn ACT Thr	CAG Gln ACT Thr CAG Gln CGG Arg GAT Asp 70	TCT Ser TGC Cys AAA Lys GCC Ala 55 TTC Phe	CCA Pro CGG Arg CCA Pro 40 TCT Ser ACA Thr	TCC Ser GCA Ala 25 GGG Gly CTC Leu	TCC Ser 10 AGT Ser AAA Lys GTC Val AAA Lys	CTG Leu CAG Gln GCC Ala CCA Pro ATC Ile 75	TCT Ser AGC Ser CCT Pro GAC Asp 60 AGC Ser	Ala ATT Ile CAG Gln 45 AGG Arg AGA Arg	AGC Ser 30 CCC Pro TTC Phe GTG Val	Val 15 AAT Asn TTG Leu AGT Ser GAG Glu	Gly TAT Tyr ATT Ile GGC Gly GCT Ala 80 TTC	96 144 192 240

Raw Sequence Listing

06/27/93 13:08:56 S5963.raw

1249																
1250	ACT TTC															324
1251	Thr Phe	_		GIĀ	Thr	Lys	Leu	_	ITe	Lys	Arg					
1252			100					105								
1253																
1254 1255	(2) TN	EODMA	TTON	T 12/01	2 (2)	2 TD	NO.	20.								
1255	(2) IN	F ORMA	LITON	T F OF	K DE	מד ה	NO:									
1257		(i) s	FOITE	יאורים	CHAI	o አ <i>ር</i> ሞነ	יסדפי	rt~c								
1258		(1) 5	-				8 am			a						
1259							o ac:			•						
1260							line									
1261			,													
1262	(:	ii) M	OLEC	CULE	TYP	E: p:	rote	in								
1263						_										
1264	(:	xi) S	EQUE	ENCE	DES	CRIP'	TION	: SE	Q ID	NO:	30:					
1265																
1266	Asp Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1267	1			5					10					15		
1268																
1269	Asp Arg	Val	Thr	Ile	Thr	Сув	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Asn	Tyr	
1270			20					25					30			
1271				_	_			_		_					_	
1272	Leu Asn	-	Tyr	Gln	Gln	Lys		Gly	Lys	Ala	Pro		Pro	Leu	Ile	
1273		35					40					45				
1274			_	_	_					_	_		-1		~ 3	
1275	Tyr Glu		Ser	Asn	Arg		ser	GTÅ	val	Pro		Arg	Pne	ser	GIĀ	
1276	50					55					60					
1277 1278	Go Gl	g.,	3 am	mh	3 -m	Dho	mb	T	T	T1.	Com	7	77a T	~1	31 -	
1278	Ser Gly 65	Ser	Авр	Int	70	Pne	IIII	rea	гув	75	per	Arg	Vai	GIU	80	
1279	0.5				, 0					, 5					00	
1281	Glu Asp	Val	Glv	Val	Tvr	Tvr	Cvs	Met	Gln	Tvr	Thr	His	Ile	Pro	Phe	
1282	Old Mbp	* u u u	013	85	-1-	- 7 -	O, D	1100	90	-3-				95		
1283																
1284	Thr Phe	Glv	Pro	Glv	Thr	Lvs	Leu	Asp	Ile	Lvs	Arg					
1285		_	100					105		•						
1286																
1287	(2) IN	FORMA	TION	FOI	R SE	Q ID	NO:	31								
1288																
1289	(i) SEQ	UENC	CE CI	HARA	CTER:	ISTI	CS:								
1290		(A) LE	ENGTI	H: 3	24 b	ase j	pair	S							
1291		-	-				aci									
1292		-	-				bot	h								
1293		(D) TC	POL	OGY:	lin	ear									
1294																
1295	(ii) MOL	ECUL	E T	YPE:	CDN	A									
1296																
1297	(iii) HYP	OTHE	STIC	AL: 1	ИО										
1298																
1299	(iv) ANT	T-SE	SNSE	: NO											
1300																

Raw Sequence Listing

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1301																	
1302		(ix)) FE	ATURI	€:												
1303			(2	A) NZ	AME/I	KEY:	CDS										
1304			(1	B) L(CAT:	ON:	1	324									
1305																	
1306																	
1307		(xi)	SE	QUEN	CE DI	ESCR:	IPTI	ON:	SEQ :	ID NO	0:31						
1308																	
1309	GAC	ATT	CAG	CTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTG	GGA	48
1310	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Glv	
1311	ī				5					10					15	•	
1312					_												
1313	GAC	ACA	GTC	ACC	ATC	ACT	TGT	CGG	GCA	AGT	CAG	GGC	ATT	AGC	AAT	AAT	96
1314							Сув										
1315				20			O, D	5	25			U -3		30			
1316				20					2,5					30			
1317	ጥጥል	acc	таа	ייעיי	CAG	CAG	AAA	CCA	CCA	222	сст	ССТ	AAG	CGC	CTC	ATC	144
1317							Lys										144
1319	пеп	AIG	35	ıyı	GIII	GIII	пув	40	GLY	цуь	ALG	FIU	45	Arg	nea	116	
1319			33					40					43				
	mam	aam	~~	maa	3 CM	mma	GAA	3 CIT	000	ama	a as	max.	100	mm/l	3 CIII	000	100
1321										-							192
1322	TYF		Ala	ser	ser	Leu	Glu	ser	GIY	vaı	Pro		Arg	Pne	ser	GIĀ	
1323		50					55					60					
1324				~~~		~			ama					~~~	~~~	~~m	240
1325							TTC										240
1326		GIY	ser	GIĀ	Thr		Phe	Thr	Leu	Thr		ser	ser	ьеп	GIN		
1327	65					70					75					80	
1328																	
1329							TAC										288
1330	Glu	Asp	Phe	Ala		Tyr	Tyr	Сув	Gln		Asp	Asn	Ser	Tyr		Phe	
1331					85					90					95		
1332																	
1333	ACT	TTC	GGC	GGA	GGG	ACC	AAG	GTG	GAG	ATC	AAA	CGA					324
1334	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
1335				100					105								
1336																	
1337																	
1338	(2)	IN	FORM	ATIO	N FOI	R SE	Q ID	NO:	32								
1339																	
1340			(i) :	SEQUI	ENCE	CHAI	RACT	ERIS:	rics	:							
1341				(A)) LEI	NGTH	: 10	8 am:	ino a	acida	3						
1342				(B)	TYI	PE: a	amin	ac:	id								
1343				(D)) TO	POLO	GY:	line	ar								
1344																	
1345		(:	ii) 1	MOLE	CULE	TYP	E: p:	rote:	in								
1346		•	, -	_	_		-										
1347		(:	xi) :	SEOUI	ENCE	DES	CRIP'	rion	: SEC	Q ID	NO:	32					
1348		,,	, .	_ = = = -					,			_					
1349	Agn	Tle	Gln	Len	Thr	Gln	Ser	Pro	Ser	Ser	Lev	Ser	Ala	Ser	Val	Glv	
1350	75p				5					10					15	1	
1351	_				3					20							
1351) en	ሞኮ <u>∽</u>	Va 1	Thr	Tle	Thr	Сув	Δνα	ء 1 ھ	Ser	Gln	Glv	٦١م	Ser	Agn	Agn	
エンフム	vaħ	TILL	val	TILL	TTG	TIII	CAB	ar A	n1d	Per	GTII	GTÅ		DGT	von	WD11	

Raw Sequence Listing

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1353			20					25					30			
1354		_	_			_	_		_			_	_			
1355	Leu Ala		Tyr	GIn	Gin	Lys		GIY	Lys	Ala	Pro		Arg	Leu	Ile	
1356		35					40					45				
1357			_	_	_		_			_	_	_				
1358	Tyr Ala		Ser	Ser	Leu		Ser	Gly	Val	Pro		Arg	Phe	Ser	Gly	
1359	50					55					60					
1360		_						_			_	_	_		_	
1361	Ser Gly	ser	GIY	Thr		Phe	Thr	Leu	Thr		Ser	Ser	Leu	Gin		
1362	65				70					75					80	
1363	~ 3 >				_	_		~-7		_	_	_	_	_		
1364	Glu Asp	Pne	Ата		ıyr	lyr	Cys	Gin		Asp	Asn	Ser	Tyr		Phe	
1365				85					90					95		
1366	_, _,				_,	_				_	_					
1367	Thr Phe	Gly	-	GTĀ	Thr	Lys	Val		Ile	Lys	Arg					
1368			100					105								
1369	(0)															
1370	(2) IN	FORMA	TIOI	N FOI	C SE) ID	NO:	33								
1371																
1372	(1) SEÇ	-													
1373				ENGTI			_	•	3							
1374		•		YPE:												
1375		•	-	FRANI				n.								
1376		(L)) T(OPOL	JGY:	line	ear									
1377	/	١ ٧٥٠		1933		-517	_									
1378	(11) MOI	'RC01	LE T	PE:	CDN	A.									
1379	,,,,	\		-m												
1380	(111) HYE	OTH	STIC	7T: I	NO										
1381		\ 3.277														
1382	(10	raa (T-21	SNSE	NO											
1383																
1384	(\ ===		-												
1385	(1X) FE#				an.a										
1386				AME/I			204									
1387		(E	3) L(CAT:	LON:	1	344									
1388																
1389	() (190	\TTE3\T/			rnm T	337 - (. OBO	FD 37	2.22						
1390	(X1) SEÇ	SORN(.B Di	SOCK.	rb.T.T(JN: 1	orų.	א חד	J: 33						
1391	CAC AMM	C A C	CTC.	3.00	C 2 C	m/Jm	CC3	TOO	TICC.	CITIC!	TT/CITT	CC3	Tr/Cim	Gm/C	CCA	10
1392	GAC ATT															48
1393 1394	Asp Ile	GIN	теп		GIU	ser	PEO	ser		ьeu	ser	WTG	ser	15	дту	
	1			5					10					13		
1395	GVG VG	CTTC	3.00	7 ma	N CITT	T C T	ccc	GC3	N CITT	C A C	aaa	7	» aa	አአጥ	שממ	96
1396	GAC ACA															90
1397 1398	Asp Thr	val		тте	Inr	cys	Arg		ber	GIH	GTÅ	тте		ASI	ARU	
1398			20					25					30			
1400	mma aaa	TOO	du y un	CAC	CNC	222	CCI	gas.	**	COm	CCM	224	CGG	CTC	አጥር	144
1400	TTA GCC															7.2.2
1401	Leu Ala	35	TÄL	GIH	GIH	пλя	40	GTÅ	пÃя	VIG	FIO	ьув 45	vr.A	пеп	TT6	
1402		33					-20					-10				
1403	TAT GCT	GCA	TCC	ልርጥ	ጥጥር፤	CAD	ልርሞ	GGG	מיזירי	CCA	ጥሮኔ	VGG	ጥጥ /ግ	ልሮጥ	GGC	192
7404	IAI GCI	GCA	100	AG1	119	GAA	AG1	G G G	GIC	COM	IÇA	AUU	110	NG I	330	192

Raw Sequence Listing

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1405	${ t Tyr}$	Ala	Ala	Ser	Ser	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
1406		50					55					60					
1407																	
1408	AGT	GGA	TCT	GGG	ACA	GAA	TTC	ACT	CTC	ACC	ATC	AGC	AGC	CTG	CAG	CCT	240
1409	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
1410	65	_		_		70					75					80	
1411																	
1412	GAA	GAT	TTT	GCA	ACT	TAT	TAC	TGT	CAA	CAG	GAT	AAC	AGT	TAT	CCT	TTC	288
1413											Asp						
1414					85	-1-	-1-	0,7		90				-1-	95		
1415					05					70					,,		
1416	λСТ	ምጥር	aac	GGA	GGG	אככ	224	CTC.	GVG	ΣΤΟ	AAA	CGA					324
1417																	324
	Thr	Pne	GIY	_	GIY	Inr	гув	val		тте	Lys	Arg					
1418				100					105								
1419																	
1420																	
1421	(2)	INI	FORM	ATIO	7 FOE	R SE(O ID	NO:	34								
1422																	
1423			(i) S	-	ENCE												
1424				(A)	LEI	GTH:	: 108	am:	ino a	acida	8						
1425				(B)	TYI	PE: 8	amino	ac:	id								
1426				(D)	TOE	POLO	3Y: :	linea	ar								
1427																	
1428		(:	ii) 1	MOLE	CULE	TYPI	נס : ב	rote	in								
1429		•	, -														
1430		(3	ci) S	TEOU	ENCE	DESC	יפדקי	TON	· SEC	מד כ	NO:	3.4					
1431		\-	, .	J-20.					,			-					
1432	7 00	T16	Gln.	Lou	Thr	Gln.	Cor	Pro	Sar	Cor	Leu	Car	בוג	Sar	17a 1	Glv	
1432	лар 1	116	GIII	Пеп	5	GIII	261	FIU	Per	10	пеа	261	AIG	Det	15	GLY	
	1				3					10					13		
1434		-1		-1		m1	a	•		a	~ 1	~1	-1 -	a	3		
1435	Asp	Thr	Val		IIe	Thr	Cys	Arg		ser	Gln	GTĀ	тте		Asn	Asn	
1436				20					25					30			
1437									_		_						
1438	Leu	Ala	\mathtt{Trp}	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro		Arg	Leu	Ile	
1439			35					40					45				
1440																	
1441	Tyr	Ala	Ala	Ser	Ser	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
1442		50					55					60					
1443																	
1444	Ser	Glv	Ser	Glv	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
1445	65			-		70					75					80	
1446	•																
1447	Glu	Aan	Dha	212	Thr	Тагт	Тъгъ	Cva	Gln	Gln	Asp	λan	Ser	Tur	Pro	Phe	
1448	GIU	roħ	L 111G	viq	85	+ y +	- A -	CyB	GTII	90	roh	WOII	DGI	-1-	95	- 110	
					00					30					33		
1449			~-	~ •	~-	1	. .		~ 1		•	3					
1450	Tnr	rne	GTĀ	_	GIY	Tnr	га	var		тте	Lys	Arg					
1451				100					105								
1452																	
1453	(2)	INI	FORM	ATIO	V FOI	R SE	O ID	NO:	35:								
1454																	
1455		(i)			CE CI												
1456			(2	A) Li	ENGTI	H: 34	42 ba	ase j	pair	8							

Raw Sequence Listing

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1457				B) T													
1458				C) S'					1								
1459			(1	D) T	OPOL	OGY:	line	ear									
1460																	
1461		(ii)	MOI	LECU	LE T	YPE:	CDN	A.									
1462																	
1463																	
1464		(ix)) FE	ATUR	E :												
1465			(2	A) N	AME/I	KEY:	CDS										
1466			(1	B) L(CAT:	ION:	1	342									
1467																	
1468																	
1469		(xi)	SE	QUEN	CE DI	ESCR:	CPTIC	on:	SEQ :	ED NO	35:35	:					
1470			,	-					-								
1471	GAC	ATT	GTG	ATG	ACT	CAG	TCT	CCA	ACT	TTC	CTT	GCT	GTG	ACA	GCA	AGT	48
1472															Ala		
1473	1				5	V				10					15		
1474	_				_												
1475	AAG	AAG	מיזירי	ACC	יייי ב	ልርጥ	TCC	ΔСТ	CCC	тст	GAG	AGC	Стт	тат	TCA	AGC	96
1476															Ser		90
1477	пув	пур	Val	20	116	per	Cyb	1111	_	per	GIU	per	neu	30	Ser	Ser	
				20					25					30			
1478		a. a		ama	a. a	m. a	mm-a	aam	maa	m. a	a. a			~~~	~~~	a. .	7.4.4
1479															GAG	-	144
1480	гав	HIS	_	vaı	HIB	Tyr	Leu		Trp	ıyr	GIN	гĀв	_	PLO	Glu	GIN	
1481			35					40					45				
1482																	
1483															GGG		192
1484	Ser		Lys	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Asn	Arg	Tyr	Ile	Gly	Val	
1485		50					55					60					
1486																	
1487	CCT	GAT	CGC	TTC	ACA	GGC	AGT	GGA	TCT	GGG	ACA	GAT	TTC	ACT	CTG	ACC	240
1488	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	
1489	65					70					75					80	
1490																	
1491	ATC	AGC	AGT	GTA	CAG	GTT	GAA	GAC	CTC	ACA	CAT	TAT	TAC	TGT	GCA	CAG	288
1492	Ile	Ser	Ser	Val	Gln	Val	Glu	Asp	Leu	Thr	His	Tyr	Tyr	Сув	Ala	Gln	
1493					85			-		90		_	-	-	95		
1494																	
1495	TTT	TAC	AGC	TAT	CCT	CTC	ACG	TTC	GGT	GCT	GGG	ACC	AAG	CTG	GAG	CTG	336
1496																	
1497		-1-		100					105		2			110			
1498																	
1499	AAA	ccc															342
1500	Lys																J
1501	пув	Arg															
1501																	
1503	/01		3055°	3 MY ^*	T 50	0.00	,	NO - 1) c .								
1504	(2)	TN	CKM	ATIO	N FOI	K SE(מדי	NU:	.00								
1505			,,,,	a = 0 =		A***		-n									
1506			(1) 8	SEQUI							_						
1507						NGTH				acida	3						
1508				(B)	TYI)	PE: a	amino	ac:	ra								

Raw Sequence Listing

06/27/93 13:09:36 S5963.raw

1509				(D)	TO	POLO	3Y: :	linea	ar							
1510																
1511		(:	ii) 1	MOLE	CULE	TYPI	3: pi	rote:	in							
1512																
1513		(2	xi) S	SEQUI	ENCE	DES	CRIP:	CION	: SE() ID	NO:	36:				
1514			_		_					_		_	_	_	_	
1515	_	Ile	Val	Met		Gln	Ser	Pro	Thr		Leu	Ala	Val	Thr		Ser
1516	1				5					10					15	
1517	,		_		_			_	_							
1518	Lys	Lys	Val		Ile	Ser	Сув	Thr		Ser	Glu	Ser	Leu		Ser	Ser
1519				20					25					30		
1520	_		_	•		_	_		_	_		_	_	_		
1521	Lys	His	Lys	Val	His	Tyr	Leu		Trp	Tyr	Gln	Lys	_	Pro	Glu	Gln
1522			35					40					45			
1523	_	_	_	_	_		_			_	_	_				
1524	Ser		Lys	Leu	Leu	Ile	_	Gly	Ala	Ser	Asn		Tyr	Ile	Gly	Val
1525		50					55					60				
1526																
1527		Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly		Asp	Phe	Thr	Leu	
1528	65					70					75					80
1529																
1530	Ile	Ser	Ser	Val	Gln	Val	Glu	Asp	Leu	Thr	His	Tyr	Tyr	Cys	Ala	Gln
1531					85					90					95	
1532																
1533	Phe	Tyr	Ser	Tyr	Pro	Leu	Thr	Phe	_	Ala	Gly	Thr	Lys	Leu	Glu	Leu
1534				100					105					110		
1535																
1536	Lys	Arg		U												
1537																
1538																
1539	(2)	INI	FORM	ATIO	7 FOI	R SE) ID	NO:	37:							
1540																
1541		(i)) SE(_												
1542				A) LI						3						
1543			(1	3) T												
1544			((C) S:	CRANI	DEDNI	ZSS:	botl	1							
1545			(1) T	OPOLO	GY:	line	ear								
1546																
1547		(ii)) MOI	LECUI	LE T	PE:	cDN2	A								
1548																
1549		(iii)	HYI	POTH	ETIC	AL: 1	10									
1550																
1551		(iv)	AN'	ri-si	ENSE	: NO										
1552																
1553																
1554		(ix)) FE	ATURI	፪:											
1555			(2	A) N	AME/I	KEY:	CDS									
1556			(1	B) L(CAT:	CON:	13	327								
1557																
1558																
1559		(xi)) SE(QUEN	CE DI	ESCR:	[PTIC	ON: S	SEQ 1	ID NO	0:37					
1560																

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1561					ACC												48
1562	Ala	Leu	Val	Met	Thr	Gln	Thr	Pro	Ala	Ser	Val	Ser	Ala	Ala	Val	Gly	
1563	1				5					10					15		
1564																	
1565	GGC	ACA	GTC	ACC	ATC	AAG	TGC	CAG	GCC	AGT	GAG	AAC	ATT	TAC	AGC	TCT	96
1566	Gly	Thr	Val	Thr	Ile	Lys	Сув	Gln	Ala	Ser	Glu	Asn	Ile	Tyr	Ser	Ser	
1567	_			20		-	-		25					30			
1568																	
1569	TTA	GCC	TGG	TAT	CAG	CAG	AAA	CCA	GGG	CAG	CCT	CCC	AAG	CTC	CTG	ATC	144
1570					Gln												
1571			35	-1-			-1-	40	1				45				
1572																	
1573	тат	ССТ	GCA	TCC	ACT	СТС	CCA	тст	ccc	CTC	CCA	TCG	cca	ጥጥር	222	GGC	192
1574					Thr												172
1575	-1-	50	****	D 01		204	55	561	GLY	Val	110	60	A. g	rne	шув	GIY	
1576		50					,,,					00					
1577	A CITT	202	TI CIT	000	ACA	CAC	ma a	» cm	OTT C	3.00	N TO C	3.00	000	ama	asa	aam.	240
1578																	240
		Arg	ser	GIY	Thr		TYP	Thr	ьеп	Thr		ser	GIY	val	GIN	_	
1579	65					70					75					80	
1580																	
1581					ACC												288
1582	GIU	Asp	Ата	Ата	Thr	Tyr	Tyr	Cys	Leu	_	ser	Asp	ser	Ser		Asp	
1583					85					90					95		
1584																	
1585	-		-		GGA												327
1586	Thr	Ala	Phe	Gly	Gly	Gly	Thr	Glu	Leu	Glu	Ile	Leu	Сув				
1587			,	100					105								
1588																	
1589																	
1590	(2)	IN	PORM	OITA	V FOI	SE(QI Q	NO:3	38:								
1591																	
1592			(i) S	SEQUI	ENCE	CHAI	RACTI	ERIST	CICS:	:							
1593				(A)	LEI	IGTH :	: 109	ami	ino a	acida	3						
1594				(B)	TYI	E: a	amino	aci	id								
1595				(D)	TOI	OLO	3Y:]	linea	ar								
1596																	
1597		(:	ii) 1	OLE	CULE	TYPE	: pi	ote	in								
1598							•										
1599		(2	ci) S	EQUI	ENCE	DESC	RIP	CION	SEC	ID C	NO:3	38:					
1600		•	•	-						•							
1601	Ala	Leu	Val	Met	Thr	Gln	Thr	Pro	Ala	Ser	Val	Ser	Ala	Ala	Val	Glv	
1602	1				5					10					15	U _1	
1603	_				_												
1604	<u>@117</u>	Th∽	v-1	Th∽	Ile	Laze	Care	G1 ~	λ 1 ο	Ge~	G1	λen	Tle	Тугъ	Ser	Co~	
1605	GIY	T 11T	Val	20	-1-G	-J O	CYB	G111	25	DGI	G1U	VOII	-14	30	DGT	261	
1605				4 U					45					30			
	T	77-	TT	Па	a 3-	61 -	T	Dece	01	~1 -	Des	Desc	T	T 6	T	T1 -	
1607	ьeu	ALA		TYT	Gln	GIN	гÃв		GТĀ	GID	PTO	PTO		ьeи	ьeu	тте	
1608			35					40					45				
1609	-			_	_,	_		_	~-		_	_	_	_,	_		
1610	Tyr	-	Ala	Ser	Thr	Leu		Ser	GТĀ	Val	Pro		Arg	Phe	ГÄЗ	GTA	
1611		50					55					60					
1612																	

Raw Sequence Listing

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1613	Ser	Arg	Ser	Gly	Thr		Tyr	Thr	Leu	Thr		Ser	Gly	Val	Gln		
1614 1615	65					70					75					80	
1616	Glu	7 an	3 1 a	%]	The s	П	П	۵.,	T 011	~1	Com	3 am	g.,,,	g	0	3	
1617	GIU	лор	ATG	AIG	85	TYL	TYL	Сув	пеп	90	Ser	App	261	Ser	95	Aab	
1618					05					30					33		
1619	Thr	λla	Pho	@1 v	G1 ₁₇	Gl ₃	Thr	Gl.	T.011	GI.	т1.	T 011	Cara				
1620	1111	AIG	FIIG	100	GIY	GLY	1111	GIU	105	GIU	116	neu	Cyb				
1621				100					103								
1622	(2)	TNI	ZODM:	י∩דיי	1 FOI	০ এছে	מד ר	NO ·	20.								
1623	(2)		· Oldin	11101	1 101	· DE	2 10	110.	,,,								
1624		(+)	SEC	TIEN	CE CE	TARA	TER	r gæ r (p		-	. ~	<i></i>				,
1625		(-)		-	INGTI						>	رے '	[/)		11.	Ste	√
1626					PE:								_		1 1.		-
1627					CRANI												
1628					POL				•								
1629			``	, -													
1630		(ii)	MOI	LECUI	LE TY	ZPE:	cDN	A									
1631		,,						-									
1632	(iii)	HYI	отн	STIC	AL: 1	10										
1633	,						_										
1634		(iv)	AN	CI-SE	ENSE	: NO											
1635		-															
1636																	
1637		(ix)	FE2	ATURI	፤ :												
1638			(2	4) N2	ME/I	KEY:	CDS										
					-												
1639			(I	3) L(CAT	CON:	13	321									
1639 1640			(I	3) L(CAT	EON:	13	321									
			(I	3) L(CAT	EON:	13	321									
1640		(xi)			CE DI				SEQ :	ED NO	D:39:	:					
1640 1641		(xi)							SEQ :	ED NO	D:39:	:					
1640 1641 1642	ACT		SEÇ	QUENC	CE DI	SCR:	[PTIC	ON: S	_				TCT	GAT	GAG	CAG	48
1640 1641 1642 1643	ACT Thr	GTG	SE(QUENC GCA	CE DI	SCR:	IPTIC GTC	ON: 8	ATC	TTC	CCG	CCA					48
1640 1641 1642 1643 1644		GTG	SE(QUENC GCA	CE DI	SCR:	IPTIC GTC	ON: 8	ATC	TTC	CCG	CCA					48
1640 1641 1642 1643 1644	Thr	GTG	SE(QUENC GCA	CE DE CCA Pro	SCR:	IPTIC GTC	ON: 8	ATC	TTC Phe	CCG	CCA			Glu		48
1640 1641 1642 1643 1644 1645	Thr	GTG Val	SE(GCT Ala	QUENO GCA Ala	CE DE CCA Pro 5	SCR: TCT Ser	GTC Val	ON: S TTC Phe	ATC Ile	TTC Phe 10	CCG Pro	CCA Pro	Ser	Asp	Glu 15	Gln	48 96
1640 1641 1642 1643 1644 1645 1646	Thr 1	GTG Val	SEG GCT Ala TCT	QUENO GCA Ala GGA	CCA Pro 5	ESCR: TCT Ser	GTC Val	ON: S TTC Phe GTT	ATC Ile	TTC Phe 10 TGC	CCG Pro	CCA Pro	Ser AAT	Asp	Glu 15 TTC	Gln TAT	
1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650	Thr 1 TTG	GTG Val	SEG GCT Ala TCT	QUENO GCA Ala GGA	CCA Pro 5	ESCR: TCT Ser	GTC Val	ON: S TTC Phe GTT	ATC Ile	TTC Phe 10 TGC	CCG Pro	CCA Pro	Ser AAT	Asp	Glu 15 TTC	Gln TAT	
1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651	Thr 1 TTG Leu	GTG Val AAA Lys	SEG GCT Ala TCT Ser	GCA Ala GGA Gly 20	CCA Pro 5 ACT Thr	TCT Ser GCC Ala	GTC Val TCT Ser	ON: S TTC Phe GTT Val	ATC Ile GTG Val 25	TTC Phe 10 TGC Cys	CCG Pro CTG Leu	CCA Pro CTG Leu	Ser AAT Asn	AAC Asn 30	Glu 15 TTC Phe	Gln TAT Tyr	96
1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650	Thr 1 TTG Leu	GTG Val AAA Lys	SE(GCT Ala TCT Ser	GCA Ala GGA Gly 20 GCC	CE DE CCA Pro 5 ACT Thr	TCT Ser GCC Ala	GTC Val TCT Ser	ON: S TTC Phe GTT Val	ATC Ile GTG Val 25	TTC Phe 10 TGC Cys	CCG Pro CTG Leu	CCA Pro CTG Leu	Ser AAT Asn GCC	AAC Asn 30	Glu 15 TTC Phe	Gln TAT Tyr TCG	
1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653	Thr 1 TTG Leu	GTG Val AAA Lys	SE(GCT Ala TCT Ser	GCA Ala GGA Gly 20 GCC	CE DE CCA Pro 5 ACT Thr	TCT Ser GCC Ala	GTC Val TCT Ser	ON: S TTC Phe GTT Val	ATC Ile GTG Val 25	TTC Phe 10 TGC Cys	CCG Pro CTG Leu	CCA Pro CTG Leu	Ser AAT Asn GCC	AAC Asn 30	Glu 15 TTC Phe	Gln TAT Tyr TCG	96
1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654	Thr 1 TTG Leu	GTG Val AAA Lys	SE(GCT Ala TCT Ser	GCA Ala GGA Gly 20 GCC	CE DE CCA Pro 5 ACT Thr	TCT Ser GCC Ala	GTC Val TCT Ser	ON: S TTC Phe GTT Val	ATC Ile GTG Val 25	TTC Phe 10 TGC Cys	CCG Pro CTG Leu	CCA Pro CTG Leu	Ser AAT Asn GCC	AAC Asn 30	Glu 15 TTC Phe	Gln TAT Tyr TCG	96
1640 1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1654 1655	Thr 1 TTG Leu CCC Pro	GTG Val AAA Lys AGA Arg	GCT Ala TCT Ser GAG Glu 35	GCA Ala GGA Gly 20 GCC Ala	CE DE CCA Pro 5 ACT Thr	TCT Ser GCC Ala GTA Val	GTC Val TCT Ser CAG Gln	ON: STTC Phe GTT Val TGG Trp 40	ATC Ile GTG Val 25 AAG Lys	TTC Phe 10 TGC Cys GTG Val	CCG Pro CTG Leu GAT Asp	CCA Pro CTG Leu AAC Asn	AAT Asn GCC Ala 45	AAC Asn 30 CTC Leu	Glu 15 TTC Phe CAA Gln	Gln TAT Tyr TCG Ser	96 144
1640 1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1654 1655 1656	Thr 1 TTG Leu CCC Pro	GTG Val AAA Lys AGA Arg	GCT Ala TCT Ser GAG Glu 35	GCA Ala GGA Gly 20 GCC Ala	CE DE CCA Pro 5 ACT Thr AAA Lys	TCT Ser GCC Ala GTA Val	GTC Val TCT Ser CAG Gln	ON: STTC Phe GTT Val TGG Trp 40	ATC Ile GTG Val 25 AAG Lys	TTC Phe 10 TGC Cys GTG Val	CCG Pro CTG Leu GAT Asp	CCA Pro CTG Leu AAC ABn	AAT Asn GCC Ala 45	AAC Asn 30 CTC Leu	Glu 15 TTC Phe CAA Gln	Gln TAT Tyr TCG Ser	96
1640 1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1654 1655 1656	Thr 1 TTG Leu CCC Pro	GTG Val AAA Lys AGA Arg	GCT Ala TCT Ser GAG Glu 35	GCA Ala GGA Gly 20 GCC Ala	CE DE CCA Pro 5 ACT Thr AAA Lys	TCT Ser GCC Ala GTA Val	GTC Val TCT Ser CAG Gln GTC Val	ON: STTC Phe GTT Val TGG Trp 40	ATC Ile GTG Val 25 AAG Lys	TTC Phe 10 TGC Cys GTG Val	CCG Pro CTG Leu GAT Asp	CCA Pro CTG Leu AAC ABn	AAT Asn GCC Ala 45	AAC Asn 30 CTC Leu	Glu 15 TTC Phe CAA Gln	Gln TAT Tyr TCG Ser	96 144
1640 1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1654 1655 1656 1657 1658	Thr 1 TTG Leu CCC Pro	GTG Val AAA Lys AGA Arg	GCT Ala TCT Ser GAG Glu 35	GCA Ala GGA Gly 20 GCC Ala	CE DE CCA Pro 5 ACT Thr AAA Lys	TCT Ser GCC Ala GTA Val	GTC Val TCT Ser CAG Gln	ON: STTC Phe GTT Val TGG Trp 40	ATC Ile GTG Val 25 AAG Lys	TTC Phe 10 TGC Cys GTG Val	CCG Pro CTG Leu GAT Asp	CCA Pro CTG Leu AAC ABn	AAT Asn GCC Ala 45	AAC Asn 30 CTC Leu	Glu 15 TTC Phe CAA Gln	Gln TAT Tyr TCG Ser	96 144
1640 1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1655 1656 1657 1658	Thr 1 TTG Leu CCC Pro	GTG Val AAA Lys AGA Arg AAC Asn 50	GCT Ala TCT Ser GAG Glu 35 TCC Ser	GCA Ala GGA Gly 20 GCC Ala CAG Gln	CE DE CCA Pro 5 ACT Thr AAA Lys GAG Glu	GCC Ala GTA Val	GTC Val TCT Ser CAG Gln GTC Val	ON: S TTC Phe GTT Val TGG Trp 40 ACA Thr	ATC Ile GTG Val 25 AAG Lys GAG Glu	TTC Phe 10 TGC Cys GTG Val CAG Gln	CCG Pro CTG Leu GAT Asp	CCA Pro CTG Leu AAC Asn	AAT Asn GCC Ala 45 AAG Lys	AAC Asn 30 CTC Leu GAC Asp	Glu 15 TTC Phe CAA Gln AGC Ser	Gln TAT Tyr TCG Ser ACC Thr	96 144 192
1640 1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1655 1655 1655 1656	Thr 1 TTG Leu CCC Pro	GTG Val AAA Lys AGA Arg AAC Asn 50	GCT Ala TCT Ser GAG Glu 35 TCC Ser	GCA Ala GGA Gly 20 GCC Ala CAG Gln	CE DE CCA Pro 5 ACT Thr AAA Lys GAG Glu	GCC Ala GTA Val AGT Ser	GTC Val TCT Ser CAG Gln GTC Val 55	ON: S TTC Phe GTT Val TGG Trp 40 ACA Thr	ATC Ile GTG Val 25 AAG Lys GAG Glu CTG	TTC Phe 10 TGC Cys GTG Val CAG Gln AGC	CCG Pro CTG Leu GAT Asp	CCA Pro CTG Leu AAC Asn AGC Ser 60	AAT Asn GCC Ala 45 AAG Lys	AAC Asn 30 CTC Leu GAC Asp	Glu 15 TTC Phe CAA Gln AGC Ser	Gln TAT Tyr TCG Ser ACC Thr	96 144
1640 1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1655 1655 1655 1656 1657 1658 1659 1660 1661	Thr 1 TTG Leu CCC Pro GGT Gly TAC Tyr	GTG Val AAA Lys AGA Arg AAC Asn 50	GCT Ala TCT Ser GAG Glu 35 TCC Ser	GCA Ala GGA Gly 20 GCC Ala CAG Gln	CE DE CCA Pro 5 ACT Thr AAA Lys GAG Glu	SCR: TCT Ser GCC Ala GTA Val AGT Ser ACC Thr	GTC Val TCT Ser CAG Gln GTC Val 55	ON: S TTC Phe GTT Val TGG Trp 40 ACA Thr	ATC Ile GTG Val 25 AAG Lys GAG Glu CTG	TTC Phe 10 TGC Cys GTG Val CAG Gln AGC	CCG Pro CTG Leu GAT Asp GAC Asp	CCA Pro CTG Leu AAC Asn AGC Ser 60	AAT Asn GCC Ala 45 AAG Lys	AAC Asn 30 CTC Leu GAC Asp	Glu 15 TTC Phe CAA Gln AGC Ser	Gln TAT Tyr TCG Ser ACC Thr	96 144 192
1640 1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1655 1655 1655 1656 1657 1660 1661 1662	Thr 1 TTG Leu CCC Pro	GTG Val AAA Lys AGA Arg AAC Asn 50	GCT Ala TCT Ser GAG Glu 35 TCC Ser	GCA Ala GGA Gly 20 GCC Ala CAG Gln	CE DE CCA Pro 5 ACT Thr AAA Lys GAG Glu	GCC Ala GTA Val AGT Ser	GTC Val TCT Ser CAG Gln GTC Val 55	ON: S TTC Phe GTT Val TGG Trp 40 ACA Thr	ATC Ile GTG Val 25 AAG Lys GAG Glu CTG	TTC Phe 10 TGC Cys GTG Val CAG Gln AGC	CCG Pro CTG Leu GAT Asp	CCA Pro CTG Leu AAC Asn AGC Ser 60	AAT Asn GCC Ala 45 AAG Lys	AAC Asn 30 CTC Leu GAC Asp	Glu 15 TTC Phe CAA Gln AGC Ser	Gln TAT Tyr TCG Ser ACC Thr	96 144 192
1640 1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1655 1655 1655 1656 1657 1658 1659 1660 1661	Thr 1 TTG Leu CCC Pro GGT Gly TAC Tyr	GTG Val AAA Lys AGA Arg AAC Asn 50 AGC Ser	GCT Ala TCT Ser GAG Glu 35 TCC Ser	GCA Ala GGA Gly 20 GCC Ala CAG Gln AGC Ser	CE DE CCA Pro 5 ACT Thr AAA Lys GAG Glu AGC Ser	GCC Ala GTA Val AGT Ser ACC Thr	GTC Val TCT Ser CAG Gln GTC Val 55 CTG Leu	ON: S TTC Phe GTT Val TGG Trp 40 ACA Thr	ATC Ile GTG Val 25 AAG Lys GAG Glu CTG Leu	TTC Phe 10 TGC Cys GTG Val CAG Gln AGC Ser	CCG Pro CTG Leu GAT Asp GAC Asp	CCA Pro CTG Leu AAC Asn AGC Ser 60 GCA Ala	AAT Asn GCC Ala 45 AAG Lys GAC Asp	AAC Asn 30 CTC Leu GAC Asp	Glu 15 TTC Phe CAA Gln AGC Ser	TAT Tyr TCG Ser ACC Thr AAA Lys 80	96 144 192

Raw Sequence Listing

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1665 1666	His	Lys	Val	Tyr	Ala 85	Сув	Glu	Val	Thr	His 90		Gly	Leu	Ser		Pro					
1667					05					30					95						
1668	GTC	ልሮል	A'AC	, AGC	didica.	220	» CC	GGA	GNG	TOT	TΓN				/			(32	-		
1669				Ser							TW				(-			(32	・ノ		
1670	Val	T 111	пув	100	FIIG	Apii	ALG	Gry	105	Cys								\sim		\sim	
1671				100					103)(
1672																		\sim	, —		
1673	(2	\ TN	RODM	ATIO	וסקו זא	D CE	חד מ	NO ·	40.									$\overline{}$	70	10-	ſ
1674	(2	, 111	ronn	A110	N PO	C DE	עד ע	110.	10.									\mathcal{A}		115-	J
1675			(i)	SEQU	RNCR	CHAI	D ል ርግጥ	RRTS	TTCQ	•										155- 15	
1676			_/				: 10				a						<u> </u>		+h	901	ſ
1677					•		amino				_							,	1 / \	ן יְרוּ.	ı
1678							GY:													,	
1679				,-,	, _0.																
1680		(ii)	MOLE	CULE	TYPI	E: p:	rote	in												
1681		`	,				-· P·														
1682		(xi)	SEQU	ENCE	DESC	CRIP	TON	· SEC	о тр	NO:	40:									
1683		`	,						,	×											
1684	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	asp	Glu	Gln					
1685	1				5					10				•	15						•
1686																					
1687	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr					
1688		-		20					25	-				30		-					
1689																					
1690	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser					
1691		_	35		-			40	_		_		45								
1692																					
1693	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr					
1694		50					55					60									
1695																					
1696	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys					
1697	65					70					75					80					
1698																					
1699	His	Lys	Val	Tyr		Сув	Glu	Val	Thr		Gln	Gly	Leu	Ser		Pro		•			
1700					85					90					95						
1701																					
1702	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly		Cys											
1703				100					105												
1704																					
1705									4 4												
1706	(2) IN	FORM	ATIO	N FOI	R SE	O ID	NO:	41:												
1707		,,	٠		am a				~~												
1708		(1		QUEN(A) L								> ~	7	\bigcirc		1	<u>چ</u> ک		1		
1709 1710				A) L: B) T:)	7		رك		1 1.	かる	e c	.		
1710			•	•																	
1711				C) 5' D) T(II												
1712			(.	ד נם	APOT(JGI:	TIME	za ſ													
1713		(44) MO:	LECU	יים ים.	VDF.	a Dati	Δ.													
1714		(11	, MO.	TECO:	ue Ti	.FB;	CDM	T.													
1715		(444) uv	POTH	emta:	AT 3	V TP C														
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Raw Sequence Listing

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Patent Application US/07/952,640

1717																	
1718		(iv)	AN'	ri-si	ense	: NO											
1719																	
1720																	
1721		(ix)) FE	ATURI	€:												
1722			()	A) NZ	AME/I	KEY:	CDS										
1723			(1	B) Lo	CAT:	CON:	1	321									
1724																	
1725																	
1726		(xi)) SE	QUEN	CE DI	SCR:	[PTI	ON:	SEQ :	ID N	0:41	:					
1727																	
1728	GCT	GTG	GCT	GCA	CCA	TCT	GTC	TTC	ATC	TTC	CCG	CCA	TCT	GAG	GAT	CAG	48
1729	Ala	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Glu	Asp	Gln	
1730	1				5					10					15		
1731																	
1732	GTG	AAA	TCT	GGA	ACT	GTC	TCT	GTT	GTG	TGC	CTG	CTG	AAT	AAC	TTC	TAT	96
1733	Val	Lys	Ser	Gly	Thr	Val	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	
1734		•		20					25	•				30		•	
1735																	
1736	CCC	AGA	GAG	GCC	AGC	GTA	AAG	TGG	AAG	GTG	GAT	GGT	GCC	CTC	AAA	ACG	144
1737				Ala													
1738		3	35					40				4	45		•		
1739																	
1740	GAT	AAC	TCC	CAG	GAG	AGT	GTC	ACA	GAG	CAG	GAC	AGC	AAG	GAC	AAC	ACC	192
1741				Gln													
1742		50					55					60	-1-				
1743																	
1744	TAC	AGC	CTG	AGC	AGC	ACC	CTG	ACG	CTG	AGC	AGC	ACA	GAC	TAC	CAG	AGT	240
1745	-		-	Ser													
1746	65	Der	Leu	Der	Der	70	Dea		Leu	561	75	****	TOP	-3-	4111	80	
1747	03					, 0					, 5					00	
1748	CAC	ልልጥ	GTC	TAT	GCC	TCC	CAA	GTC	ACC	СУТ	CAG	GGC	СТС	AGC	TCG	כככ	288
1749				Tyr													200
1750	1110	AOII	VAI	-7-	85	Cyb	GIU	401	1111	90	GIII	GLY	164	561	95	110	
1751					03					70					,,		
1752	GT/C	»cc	AAG	AGC	Trape	224	» CC	CCA	CAC	тст	тλ						(321)
1753				Ser													$\begin{pmatrix} 321 \\ 2 \end{pmatrix} $
1754	Val	1111	пуь	100	FIIG	ADII	ALG	GLY	105	Cyb							2500
1755				100					103								
1756																	
1757	(2)	TNI	FODM:	ATIOI	v F∩i	9 Q TP (מד ר	NO ·	12.								
1758	(4)	, 1147	CKM	AIIOI	N FOI	, obj	2 ID	110.	14.								
1759			(4) (SEQUI	rnce	ימעי	יחיי) ע כ	PDTC	rt <i>ce</i>								
1760			(- /)		ENCE) LEI												·
1761) TYI					AC T U	•						
1761) TO												
1762				(D)	, 101	OHO	31: .	r T (16)	21								
1763 1764		,		MOT TO	ים זוור	пил	P										
1764 1765		(:	TT) 1	MOLE	CULE	TIPI	r: b:	LUCE	LII								
1765 1766		,_	٠ ١ ١ ٠	יייסקי	ence	DEC	יתדמר	PT/NT) TD	NO	12-					
		(2	Kl)	SEQUI	FNCE	משת)	KTP.	TTON	: SE	מדי	NO:	14:					
1767																	

1768 Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Glu Asp Gln

Raw Sequence Listing

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1769	1				5					10					15		
1770 1771	Val	Lys	Ser	Glv	Thr	Val	Ser	Val	Val	Cvs	Leu	Leu	Aan	Asn	Phe	Tvr	
1772				20					25	-2-				30		-4-	
1773																	
1774	Pro	Arg		Ala	Ser	Val	Lys	_	Lys	Val	Asp	Gly		Leu	Lys	Thr	
1775			35					40					45				
1776 1777	3	3	C	a1 -	~1	o	77-7	mb	~1	71 -	3	C	7	3	3	mb	
1778	ABD	Asn 50	ser	GIII	GIU	ser	55	THE	GIU	GIII	Авр	60	гув	Авр	ABII	Inr	
1779		30					33					00					
1780	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Ser	Thr	Asp	Tyr	Gln	Ser	
1781	65					70					75		•	•		80	
1782																	
1783	His	Asn	Val	Tyr	Ala	Сув	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	
1784					85					90					95		
1785					_			_	_								
1786	Val	Thr	Lys		Phe	Asn	Arg	Gly		Сув							
1787				100					105								
1788 1789																	
1790	(2)) INI	PORM	וחדת	ION V	2 SE(מד כ	NO:	43.								
1791	\ 2	,	. 0.44				2	1.0.									
1792		(i)) SE	QUEN	CE CE	LARA	CTER:	ISTIC	cs:		_		, /	٦.			1
1793					engti					8	> (54		ク	-)	$' \sim .$	ted
1794			(1	B) T	YPE:	nuc	leic	acio	<u>a</u>					_	•	. —	.,
1795					rani				h								
1796			(1	D) T	OPOL	OGY:	line	ear									
1797		,															
1798 1799		(11)	MOI	PRCA:	LE T	rpe:	CDM	A.									
1800		(iii)	HVI	ротн	RTTC:	ΔT. • 1	NΟ										
1801		(
1802		(iv)	AN'	ri-si	ENSE	: NO											
1803																	
1804																	
1805		(ix)) FE	ATUR	E:												
1806					AME/I												
1807			(1	B) L	OCAT:	CON:	1	321									
1808																	
1809 1810		(sed)	CE/	ATTENT/	ית שי	ze∕rb.	TDTT	ANT.	ero .	TD N	0:43						
1811		(AL	, oe	SOBIA(ו/נו בני	JUCK.	-E T T (J14 : 1	Juy .	-D 14(J. I J	•					
1812	GAT	CCA	ATT	GCG	CCT	ACT	GTC	CTC	CTC	TTC	CCA	CCA	TCT	GCT	GAT	CAG	48
1813		Pro															
1814	1				5					10					15		
1815																	
1816		ACA															96
1817	Leu	Thr	Thr		Thr	Val	Thr	Ile		Сув	Val	Ala	Asn	_	Phe	Arg	
1818				20					25					30			
1819	000	AAT	a	3 000	200	CITIC C	3.00	THO CO	7 7 C	CTC	GλT	G A G	CD P	እጥሮ	(7 A A	CNC	144
1820	CCC	AAT	GAC	AIC	ACC	GIC	ACC	IGG	AAG	GIG	GAT	GAC	GAA	MIÇ	CAM	CAG	144

Raw Sequence Listing

06/27/93 13:10:17 S5963.raw

1821 1822	Pro	Asn	Asp 35	Ile	Thr	Val	Thr	Trp	Lys	Val	Asp	Asp	Glu 45	Ile	Gln	Gln	
1823																	
1824	AGC	GGC	TTC	GAG	AAC	AGT	ACA	ACA	CCG	CAG	AGC	CCC	GAG	GAC	TGT	ACC	192
1825	Ser	Gly	Phe	Glu	Asn	Ser	Thr	Thr	Pro	Gln	Ser	Pro	Glu	Asp	Сув	Thr	
1826		50					55					60		_	_		
1827																	
1828	TAC	AAC	CTC	AGC	AGC	ACT	CTG	TCA	CTG	ACC	AAA	GCA	CAG	TAC	AAC	AGC	240
1829	Tyr	Asn	Leu	Ser	Ser	Thr	Leu	Ser	Leu	Thr	Lys	Ala	Gln	Tyr	Asn	Ser	
1830	- 65					70					- 75			-		80	
1831																	
1832	CAC	AGC	GTG	TAC	ACC	TGC	GAG	GTG	GTC	CAT	CAC	AAC	TCG	GGC	TCA	GCG	288
1833	His	Ser	Val	Tyr	Thr	Сув	Glu	Val	Val	His	His	Asn	Ser	Gly	Ser	Ala	
1834				•	85	•				90				-	95		
1835																	
1836	ATC	GTC	CAG	AGC	TTC	AAT	AGG	GGT	GAC	TGT	TA						/ 321
1837	Ile	Val	Gln	Ser	Phe	Asn	Arg	Gly	Asp	Сув							
1838				100			_	•	105	•							
1839																	
1840																	
1841	(2)	INI	FORM	ATIO	I FOI	R SEC	O ID	NO:4	14:								
1842	ι - ,					,											
1843			(i) 9	SEOUI	ENCE	CHAI	RACTI	ERIS:	rics:	:							
1844			, -	~		IGTH:					3						
1845						PE: a											
1846				(D)	TOI	POLOC	3Y:]	linea	ar								
1846 1847				(D)	TOI	POLO	GY:]	linea	ar								
1847		(:	ii) 1														
1847 1848		(:	ii) 1	(D)													
1847 1848 1849				MOLE	CULE	TYPI	3: pı	rote:	in) ID	NO:4	14:					
1847 1848 1849 1850					CULE	TYPI	3: pı	rote:	in) ID	NO:	14:					
1847 1848 1849 1850 1851	Asp	(2	κi) S	MOLE(CULE ENCE	TYPI DESC	3: pi	rote: TION:	in : SE(Ser	Ala	Asp	Gln	
1847 1848 1849 1850 1851 1852	-	(2	κi) S	MOLE	CULE ENCE	TYPI DESC	3: pi	rote: TION:	in : SE(Phe			Ser	Ala	_	Gln	
1847 1848 1849 1850 1851 1852 1853	Asp 1	(2	κi) S	MOLE(CULE ENCE Pro	TYPI DESC	3: pi	rote: TION:	in : SE(Ser	Ala	Asp 15	Gln	
1847 1848 1849 1850 1851 1852 1853 1854	ĩ	(z	ki) S	MOLEC SEQUI Ala	ENCE Pro 5	TYPI DESC	S: pr CRIPT Val	rote: TION: Leu	in : SE(Leu	Phe 10	Pro	Pro			15		
1847 1848 1849 1850 1851 1852 1853 1854 1855	ĩ	(z	ki) S	MOLEG SEQUI Ala Glu	ENCE Pro 5	TYPI DESC	S: pr CRIPT Val	rote: TION: Leu	in : SEÇ Leu Val	Phe 10	Pro	Pro			15		
1847 1848 1849 1850 1851 1852 1853 1854 1855	ĩ	(z	ki) S	MOLEC SEQUI Ala	ENCE Pro 5	TYPI DESC	S: pr CRIPT Val	rote: TION: Leu	in : SE(Leu	Phe 10	Pro	Pro		Lys	15		
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856	1 Leu	Pro Thr	ki) S Ile Thr	MOLEG SEQUE Ala Glu 20	CULE ENCE Pro 5	TYPE DESC Thr	S: processor pro	rote: FION: Leu Ile	in : SEÇ Leu Val 25	Phe 10 Cys	Pro Val	Pro Ala	Asn	Lys 30	15 Phe	Arg	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857	1 Leu	Pro Thr	ci) s Ile Thr	MOLEG SEQUI Ala Glu	CULE ENCE Pro 5	TYPE DESC Thr	S: processor pro	rote: FION: Leu Ile	in : SEÇ Leu Val 25	Phe 10 Cys	Pro Val	Pro Ala	Asn Glu	Lys 30	15 Phe	Arg	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858	1 Leu	Pro Thr	ki) S Ile Thr	MOLEG SEQUE Ala Glu 20	CULE ENCE Pro 5	TYPE DESC Thr	S: processor pro	rote: FION: Leu Ile	in : SEÇ Leu Val 25	Phe 10 Cys	Pro Val	Pro Ala	Asn	Lys 30	15 Phe	Arg	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860	1 Leu Pro	Pro Thr	Ile Thr Asp	MOLEG SEQUI Ala Glu 20 Ile	Pro 5 Thr	TYPE DESC Thr Val	S: process of the control of the con	rote: FION: Leu Ile Trp 40	in : SEG Leu Val 25 Lys	Phe 10 Cys	Pro Val Asp	Pro Ala Asp	Asn Glu 45	Lys 30 Ile	15 Phe Gln	Arg Gln	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861	1 Leu Pro	Pro Thr Asn	Ile Thr Asp	MOLEG SEQUE Ala Glu 20	Pro 5 Thr	TYPE DESC Thr Val	ERIPT Val Thr Thr	rote: FION: Leu Ile Trp 40	in : SEG Leu Val 25 Lys	Phe 10 Cys	Pro Val Asp	Pro Ala Asp	Asn Glu 45	Lys 30 Ile	15 Phe Gln	Arg Gln	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862	1 Leu Pro	Pro Thr	Ile Thr Asp	MOLEG SEQUI Ala Glu 20 Ile	Pro 5 Thr	TYPE DESC Thr Val	S: process of the control of the con	rote: FION: Leu Ile Trp 40	in : SEG Leu Val 25 Lys	Phe 10 Cys	Pro Val Asp	Pro Ala Asp	Asn Glu 45	Lys 30 Ile	15 Phe Gln	Arg Gln	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862	1 Leu Pro Ser	Pro Thr Asn Gly 50	Thr Asp 35	MOLEG SEQUI Ala Glu 20 Ile Glu	ENCE Pro 5 Thr Thr	TYPE DESC Thr Val Val	Z: process of the control of the con	rote: FION: Leu Ile Trp 40 Thr	in : SE(Leu Val 25 Lys	Phe 10 Cys Val	Pro Val Asp	Pro Ala Asp Pro 60	Asn Glu 45 Glu	Lys 30 Ile Asp	15 Phe Gln Cys	Arg Gln Thr	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864	1 Leu Pro Ser	Pro Thr Asn Gly 50	Thr Asp 35	MOLEG SEQUI Ala Glu 20 Ile	ENCE Pro 5 Thr Thr	TYPE DESC Thr Val Val Ser	Z: process of the control of the con	rote: FION: Leu Ile Trp 40 Thr	in : SE(Leu Val 25 Lys	Phe 10 Cys Val	Pro Val Asp Ser	Pro Ala Asp Pro 60	Asn Glu 45 Glu	Lys 30 Ile Asp	15 Phe Gln Cys	Arg Gln Thr	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865	1 Leu Pro Ser	Pro Thr Asn Gly 50	Thr Asp 35	MOLEG SEQUI Ala Glu 20 Ile Glu	ENCE Pro 5 Thr Thr	TYPE DESC Thr Val Val	Z: process of the control of the con	rote: FION: Leu Ile Trp 40 Thr	in : SE(Leu Val 25 Lys	Phe 10 Cys Val	Pro Val Asp	Pro Ala Asp Pro 60	Asn Glu 45 Glu	Lys 30 Ile Asp	15 Phe Gln Cys	Arg Gln Thr	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866	1 Leu Pro Ser Tyr 65	Pro Thr Asn Gly 50 Asn	Thr Asp 35 Phe	MOLEG SEQUI Ala Glu 20 Ile Glu Ser	CULE Pro 5 Thr Asn Ser	TYPE DESC Thr Val Val Ser Thr 70	CRIPT Val Thr Thr 55	rote: FION: Leu Ile Trp 40 Thr	in ESE Leu Val 25 Lys Pro Leu	Phe 10 Cys Val Gln	Pro Val Asp Ser Lys 75	Pro Ala Asp Pro 60 Ala	Asn Glu 45 Glu Gln	Lys 30 Ile Asp	15 Phe Gln Cys Asn	Arg Gln Thr Ser	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867	1 Leu Pro Ser Tyr 65	Pro Thr Asn Gly 50 Asn	Thr Asp 35 Phe	MOLEG SEQUI Ala Glu 20 Ile Glu	CULE Pro 5 Thr Thr Asn Ser	TYPE DESC Thr Val Val Ser Thr 70	CRIPT Val Thr Thr 55	rote: FION: Leu Ile Trp 40 Thr	in ESE Leu Val 25 Lys Pro Leu	Phe 10 Cys Val Gln Thr	Pro Val Asp Ser Lys 75	Pro Ala Asp Pro 60 Ala	Asn Glu 45 Glu Gln	Lys 30 Ile Asp	15 Phe Gln Cys Asn	Arg Gln Thr Ser	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868	1 Leu Pro Ser Tyr 65	Pro Thr Asn Gly 50 Asn	Thr Asp 35 Phe	MOLEG SEQUI Ala Glu 20 Ile Glu Ser	CULE Pro 5 Thr Asn Ser	TYPE DESC Thr Val Val Ser Thr 70	CRIPT Val Thr Thr 55	rote: FION: Leu Ile Trp 40 Thr	in ESE(Leu Val 25 Lys Pro Leu	Phe 10 Cys Val Gln	Pro Val Asp Ser Lys 75	Pro Ala Asp Pro 60 Ala	Asn Glu 45 Glu Gln	Lys 30 Ile Asp	15 Phe Gln Cys Asn	Arg Gln Thr Ser	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868	1 Leu Pro Ser Tyr 65 His	Pro Thr Asn Gly 50 Asn	Thr Asp 35 Phe Leu Val	MOLEG SEQUI Ala Glu 20 Ile Glu Ser	ENCE Pro 5 Thr Thr Asn Ser Thr 85	TYPE DESC Thr Val Val Ser Thr 70	CRIPT Val Thr Thr 55 Leu Glu	TION: Leu Ile Trp 40 Thr Ser	in : SE(Leu Val 25 Lys Pro Leu Val	Phe 10 Cys Val Gln Thr	Pro Val Asp Ser Lys 75	Pro Ala Asp Pro 60 Ala	Asn Glu 45 Glu Gln	Lys 30 Ile Asp	15 Phe Gln Cys Asn	Arg Gln Thr Ser	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870	1 Leu Pro Ser Tyr 65 His	Pro Thr Asn Gly 50 Asn	Thr Asp 35 Phe Leu Val	MOLEG SEQUI Ala Glu 20 Ile Glu Ser Tyr	ENCE Pro 5 Thr Thr Asn Ser Thr 85	TYPE DESC Thr Val Val Ser Thr 70	CRIPT Val Thr Thr 55 Leu Glu	TION: Leu Ile Trp 40 Thr Ser	in ESECTION Leu Val Pro Leu Val Asp	Phe 10 Cys Val Gln Thr	Pro Val Asp Ser Lys 75	Pro Ala Asp Pro 60 Ala	Asn Glu 45 Glu Gln	Lys 30 Ile Asp	15 Phe Gln Cys Asn	Arg Gln Thr Ser	
1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868	1 Leu Pro Ser Tyr 65 His	Pro Thr Asn Gly 50 Asn	Thr Asp 35 Phe Leu Val	MOLEG SEQUI Ala Glu 20 Ile Glu Ser	ENCE Pro 5 Thr Thr Asn Ser Thr 85	TYPE DESC Thr Val Val Ser Thr 70	CRIPT Val Thr Thr 55 Leu Glu	TION: Leu Ile Trp 40 Thr Ser	in : SE(Leu Val 25 Lys Pro Leu Val	Phe 10 Cys Val Gln Thr	Pro Val Asp Ser Lys 75	Pro Ala Asp Pro 60 Ala	Asn Glu 45 Glu Gln	Lys 30 Ile Asp	15 Phe Gln Cys Asn	Arg Gln Thr Ser	



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1873																		
1874																		
1875	(2)) IN	FORM	ATIO	N FO	R SE	QID	NO:	45:									
1876																		
1877		(i)		QUEN							1							
1878				A) LI					_	B					7	(l	mee	
1879			•	B) T								_	_	•			\mathcal{I}	
1880			•	C) S:					h									
1881			(1	D) T	OPOL	OGY:	lin	ear										
1882																		
1883		(ii)) MO	LECU	LE T	YPE:	CDN	A										
1884																		
1885		(iii)	HY:	POTH	ETIC	AL: 1	07/											
1886																		
1887		(iv)) AN	ri-si	ENSE	: NO												
1888																		
1889																		
1890		(ix)		ATURI														
1891			(2	A) N	AME/I	KEY:	CDS											
1892			(1	B) L(OCAT:	ION:	1	321										
1893																		
1894																		
1895		(xi)) SE	QUEN	CE DI	ESCR:	IPTI	ON:	SEQ :	ID N	0:45	:						
1896																		
1897	GCT	GAT	GCT	GCA	CCA	ACT	GTA	TCC	ATC	TTC	CCA	CCA	TCC	AGT	GAG	CAG	48	
1898	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro	Ser	Ser	Glu	Gln		
1899	1				5					10					15			
1900																		
1901	TTA	ACA	TCT	GGA	GGT	GCC	TCA	GTC	GTG	TGC	TTC	TTG	AAC	AAC	TTC	TAC	96	
1902	Leu	Thr	Ser	Gly	Gly	Ala	Ser	Val	Val	Сув	Phe	Leu	Asn	Asn	Phe	Tyr		
1903				20					25					30				
1904																		
1905	CCC	AAA	GAC	ATC	AAT	GTC	AAG	TGG	AAG	ATT	GAT	GGC	AGT	GAA	CGA	CAA	144	
1906	Pro	Lys	Asp	Ile	Asn	Val	Lys	Trp	Lys	Ile	Asp	Gly	Ser	Glu	Arg	Gln		
1907			35					40					45					
1908																		
1909	AAT	GGC	GTC	CTG	AAC	AGT	TGG	ACT	GAT	CAG	GAC	AGC	AAA	GAC	AGC	ACC	192	
1910	Asn	Gly	Val	Leu	Asn	Ser	Trp	Thr	Asp	Gln	Asp	Ser	Lys	Asp	Ser	Thr		
1911		50					55					60						
1912																		
1913	TAC	AGC	ATG	AGC	AGC	ACC	CTC	ACG	TTG	ACC	AAG	GAC	GAG	TAT	GAA	CGA	240	
1914	Tyr	Ser	Met	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Lys	Asp	Glu	Tyr	Glu	Arg		
1915	65					70					75					80		
1916																		
1917	CAT	AAC	AGC	TAT	ACC	TGT	GAG	GCC	ACT	CAC	AAG	ACA	TCA	ACT	TCA	CCC	288	
1918	His	Asn	Ser	Tyr	Thr	Сув	Glu	Ala	Thr	His	Lys	Thr	Ser	Thr	Ser	Pro		
1919				•	85	•				90	•				95			
1920																		
1921	ATT	GTC	AAG	AGC	TTC	AAC	AGG	AAT	GAG	TGT	TA						321	
1922				Ser														
1923			• -	100			-		105	•								
1924																		
																		

Raw Sequence Listing

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1925																
1926	(2)) IN	FORM	ATIO	N FO	R SE	Q ID	NO:	46:							
1927																
1928			(i)	SEQU	ENCE	CHA	RACT	ERIS'	rics	:						
1929				(A)) LE	NGTH	: 10	6 am :	ino a	acid	3					
1930				(B)	TY:	PE: a	amino	o ac	id							
1931				(D	TO:	POLO	GY: :	line	ar							
1932																
1933		(ii) 1	MOLE	CULE	TYP	E: p:	rote	in							
1934		·	-				•									
1935		(:	xi) s	SEOU	ENCE	DES	CRIP'	rion	: SEC	O ID	NO:	46:				
1936		•	•	~					,	•						
1937	Ala	asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro	Ser	Ser	Glu	Gln
1938	1				5					10					15	
1939					_											
1940	Leu	Thr	Ser	Glv	Glv	Ala	Ser	Val	Val	Cvs	Phe	Leu	Asn	Asn	Phe	Tvr
1941				20	2				25	-1-				30		-1-
1942																
1943	Pro	Lvs	Asp	Ile	Asn	Val	Lvs	Tro	Lvs	Ile	Asp	Glv	Ser	Glu	Ara	Gln
1944		-1-	35				-,-	40	-7-			1	45		5	 -
1945								- •								
1946	Asn	Glv	Val	Leu	Asn	Ser	Tro	Thr	Asp	Gln	Asp	Ser	Lvs	Asp	Ser	Thr
1947		50					55					60	-1-			
1948																
1949	Tvr	Ser	Met	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Lvs	Asp	Glu	Tvr	Glu	Ara
1950	65					70					75			-1-		80
1951	•					. •					. •					
1952	His	Asn	Ser	Tvr	Thr	Cvs	Glu	Ala	Thr	His	Lvs	Thr	Ser	Thr	Ser	Pro
1953				-1-	85	- 22.				90	-1-				95	
1954					43											
1955	Tle	Val	Lvs	Ser	Phe	Agn	Δτα	Agn	Glu	Cve						
1956	116	va_	-Jy 6	100	- MC	AOII	ni 9	ASII	105	Cyb						
1957				T00					103							
133/																

PAGE: 1

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/07/952,640

DATE: 06/27/93 TIME: 13:10:31

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LINE ERROR ORIGINAL TEXT

28	Wrong application Serial Number	(A) APPLICATION NUMBER: US 07/952640
572	Wrong Amino Acid Designator	210 215 (2) INFORMA
572	Wrong Amino Acid Designator	210 215 (2) INFORMA
572	Wrong Amino Acid Designator	210 215 (2) INFORMA
572	Wrong Amino Acid Designator	210 215 (2) INFORMA
572	Wrong Amino Acid Designator	210 215 (2) INFORMA
572	Wrong Amino Acid Designator	210 215 (2) INFORMA
592	Wrong Sequence Number	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
623		Sequence 13 missing
1642	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
1726	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
1810	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
1895	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
11	Number of Sequences Doesn't Equal Actual	(iii) NUMBER OF SEQUENCES: 46

PAGE: 1

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/07/952,640

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MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA APPLICATION NUMBER FILING DATE

PAGE:

SEQUENCE CORRECTION REPORT PATENT APPLICATION US/07/952,640

DATE: 06/27/93 TIME: 13:10:31

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LINE ORIGINAL TEXT

1

1287 (2) INFORMATION FOR SEQ ID NO:31

1307 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

1338 (2) INFORMATION FOR SEQ ID NO:32

1347 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

1370 (2) INFORMATION FOR SEQ ID NO:33

1390 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

1421 (2) INFORMATION FOR SEQ ID NO:34

1430 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

1559 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

CORRECTED TEXT

(2) INFORMATION FOR SEQ ID NO:31:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

(2) INFORMATION FOR SEQ ID NO:32:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:32:

(2) INFORMATION FOR SEQ ID NO:33:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

(2) INFORMATION FOR SEQ ID NO:34:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37: